

A>Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A/Reference number: A82515; MUID:20365717; PMID:10910347
A/Note: for a complete list of authors see reference number A59328 below

A/Accession: C82713
A>Status: preliminary
A/Molecule type: DNA
A/Residues: 1-433 <SIM>
A/Cross-references: GB:AE003952; GB:AE003849; NID:g9106147; FIDN:AAF83993.1; GSPDB:GN001
R/Simpon, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A.
Briones, M.R.S.; Bueno, M.R.P.; Canagao, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carver, H.
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000

A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A/Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
M.; Tshako, da Silva, A.C.R.; da Silva, P.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
A/Reference number: A59328
A/Contents: annotation
C/Genetics:
A/Gene: XF1183
C/Superfamily: UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase

Query Match 22.8%; Score 52; DB 2; Length 433;
Best Local Similarity 41.9%; Pred. No.25;
Matches 13; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

Qy 15 LVVFLVLQISLGLDIDSRTFAEVCATHTIS 45
| | | | | : | | | | : | | | | :
Db 29 LAVAFGRQPTLGFDIDICRVQLCGAGHDIT 59

RESULT 6
C86206
hypothetical protein [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
R/Theologis, A.; Eckert, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.,
anster, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luo, J.S.; Maili, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A86141; MUID:21016719; PMID:11130712
A/Accession: C86206
A>Status: preliminary
A/Molecule type: DNA
A/Residues: 1-155 <STO>
A/Cross-references: GB:AE005172; NID:g8954033; PIDN:AAF82207.1; GSPDB:GN00141
C/Genetics:
A/Map position: 1

Query Match 22.6%; Score 51.5; DB 2; Length 155;
Best Local Similarity 33.3%; Pred. No.11;
Matches 13; Conservative 7; Mismatches 18; Indels 1; Gaps 1;

Qy 8 LRNRQFTLLVFLVLQISLGLDIDSRTFAEVCATHTISP 46
| | | | | : | | | | : | | | | :
Db 3 LRRTWLVIYLFIHFLQHNLPSVSRRPSS-VDTNHETLP 40

RESULT 7
Acg7775
protein-export membrane protein SECG [imported] - Agrobacterium tumefaciens (strain C58),

```

;Species: Agrobacterium tumefaciens
;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
;Accession: AG2775
;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
;Rage, G.; Gillet, P.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
;Karp, P.; Romero, P.; Zhang, S.
;Science 294, 2317-2323, 2001
;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
;ter, E.W.
;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
;Reference number: AB2577; MUID:21608550; PMID:11743193
;Accession: AG2775
;Status: preliminary
;Molecule type: DNA
;Residues: 1-157 <KUR>
;Cross-references: GB:AE008698; PIDN:AL42621.1; PID:gl7740050; GSPDB:GN00186
;Experimental source: strain C58 (Dupont)
;Genetics:
;Gene: secG
;Map position: circular chromosome

Query Match 22.4%; Score 51; DB 2; Length 157;
Best Local Similarity 45.7%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 15; Indels 2; Gaps 1;

Y 3 GFASLLRNQFILLVFLFLLQIQSLGL--DIDSRT 35
D 43 GTANALRTTGCILAAALFFLSGLGLMTRVRSRT 77

RESULT 8
397535
;Species: Agrobacterium tumefaciens
;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
;Accession: E97555
;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
;A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
;Science 294, 2323-2328, 2001
;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
;Reference number: A97359; MUID:21608551; PMID:11743194
;Accession: E97555
;Status: preliminary
;Molecule type: DNA
;Residues: 1-162 <KUR>
;Cross-references: GB:AB007869; PIDN:AAK87398.1; PID:gl5156708; GSPDB:GN00169
;Genetics:
;Gene: AGR_C 2986
;Map position: circular chromosome

Query Match 22.4%; Score 51; DB 2; Length 162;
Best Local Similarity 45.7%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 15; Indels 2; Gaps 1;

Y 3 GFASLLRNQFILLVFLFLLQIQSLGL--DIDSRT 35
D 48 GTANALRTTGCILAAALFFLSGLGLMTRVRSRT 82

RESULT 9
H81996
;Species: Agrobacterium tumefaciens
;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
;Accession: H81996
;R.Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
;Hollroyd, S.; Jagels, K.; Leather, S.; Mungall, K.; Quail, M.A.; Rajandream,
;Nature 404, 502-506, 2000
;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
;Reference number: AB1775; MUID:2022556; PMID:10761919
;Accession: H81996
;Status: preliminary
;Molecule type: DNA

;Species: Agrobacterium tumefaciens
;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
;Accession: AG2775
;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
;Rage, G.; Gillet, P.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
;Karp, P.; Romero, P.; Zhang, S.
;Science 294, 2317-2323, 2001
;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
;ter, E.W.
;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
;Reference number: AB2577; MUID:21608550; PMID:11743193
;Accession: AG2775
;Status: preliminary
;Molecule type: DNA
;Residues: 1-157 <KUR>
;Cross-references: GB:AE008698; PIDN:AL42621.1; PID:gl7740050; GSPDB:GN00186
;Experimental source: strain C58 (Dupont)
;Genetics:
;Gene: secG
;Map position: circular chromosome

Query Match 22.4%; Score 51; DB 2; Length 328;
Best Local Similarity 44.7%; Pred. No. 26;
Matches 17; Conservative 4; Mismatches 11; Indels 6; Gaps 1;

QY 10 RNQFILLVFLFLL-----QIQSLGLDIDSRTAEVCAT 41
DB 99 RNTLLLVLFSLAFIWSAQIQTLALSMFAVAAVVAT 136

RESULT 10
E81225
;Species: Neisseria meningitidis
;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
;Accession: E81225
;R.Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.J.
;Hickey, E.K.; Hatt, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
;ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
;Science 287, 1809-1815, 2000
;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
;Reference number: AB1000; MUID:20175755; PMID:10710307
;Accession: E81225
;Status: preliminary
;Molecule type: DNA
;Residues: 1-328 <TET>
;Cross-references: GB:AE002378; GB:AE002098; NID:g7225428; PIDN:AAF40669.1; PID:g722543
;Experimental source: serogroup B, strain MC58
;Genetics:
;Gene: NMB0213
;Superfamily: Neisseria meningitidis probable integral membrane protein NMA0055

Query Match 22.4%; Score 51; DB 2; Length 328;
Best Local Similarity 44.7%; Pred. No. 26;
Matches 17; Conservative 4; Mismatches 11; Indels 6; Gaps 1;

QY 10 RNQFILLVFLFLL-----QIQSLGLDIDSRTAEVCAT 41
DB 99 RNTLLLVLFSLAFIWSAQIQTLALSMFAVAAVVAT 136

RESULT 11
T28926
;Species: Caenorhabditis elegans
;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
;Accession: T28926
;Stellives, L.
;Submitted to the EMBL Data Library, May 1996
;Description: The sequence of C. elegans cosmid F20B4.
;Reference number: Z20529
;Accession: T28926
;Status: preliminary; translated from GB/EMBL/DBJ
;Molecule type: DNA
;Residues: 1-337 <STE>
;Cross-references: EMBL:U59735; PIDN:AAC48143.1; GSPDB:GN00028; CESP:F20B4.2
;Experimental source: strain Bristol N2; clone F20B4
;Genetics:
;Gene: CESP:F20B4.2
;Map position: X

Query Match 22.4%; Score 51; DB 2; Length 337;
Best Local Similarity 32.1%; Pred. No. 27;
Matches 9; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 17 VFLFLLQIQSLGLDIDSRTAEVCATHTI 44
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Db 55 IYVTLSTDNSILDIDHQPKEIAFTSL 82

RESULT 12

JC7389
Thyroid stimulating hormone receptor a - salmon
A:Alternate names: thyrotropin receptor a
C:Species: Oncorhynchus sp. (salmon)
C>Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 07-Mar-2003
C:Accession: JC7389
A:Authors: Y. Hirai, T.; Yoshiura, Y.; Kobayashi, T.; Nagahama, Y.
A:Title: Cloning, functional characterization, and expression of thyrotropin receptors
A:Reference number: JC7389
A:Contents: Thyroid
A:Molecule type: mRNA
A:Accession: JC7389
A:Residues: 1-814 <ORA>
A:Cross-references: DDBJ:AB030954
C:Comment: This receptor, a transmembrane protein, which mediates the actions of thyrotropin
C:Genetics:
A:Gene: tsh-ra
A:Introns: 610/3
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat h
C:Keywords: glycoprotein; hormone receptor; thyroid gland; transmembrane protein

Query Match 22.4%; Score 51; DB 2; Length 814;
Best Local Similarity 47.1%; Pred. No. 64;
Matches 16; Conservative 4; Mismatches 10; Indels 4; Gaps 2;

QY 15 LVLFLQLQSLGLDIDSRPTAEVCA---THTIS 45
Db 16 LFTLVTLPIKILG-DTDSCTVCSSEWKIVTIS 48

RESULT 13

T20579
Hypothetical protein F46C3.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T20579; T22299
R:Dobson, R.
Submitted to the EMBL Data Library, November 1995
A:Reference number: Z19295
A:Accession: T20579
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1077 <WIL>
A:Cross-references: EMBL:Z68104; PIDN:CAA92117.1; GSPDB:GN00028; CESP:F46C3.1
A:Experimental source: clone F08B12
R:Cottage, A.
Submitted to the EMBL Data Library, November 1995
A:Reference number: Z19543
A:Accession: T22299
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1077 <W12>
A:Cross-references: EMBL:Z66563; PIDN:CAA91470.1; GSPDB:GN00028; CESP:F46C3.1
A:Experimental source: clone F46C3
C:Genetics:
A:Gene: CESP:F46C3.1
A:Map position: X
A:Introns: 38/3; 93/3; 272/3; 365/1; 422/1; 507/3; 541/3; 640/2; 764/1; 855/3; 922/2; 10

Query Match 22.4%; Score 51; DB 2; Length 1077;
Best Local Similarity 54.2%; Pred. No. 84;
Matches 13; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY 19 FLQLQSLGLDIDSRPTAEVCA 42
Db 1052 FLQLQSLGLDIDSRPTAEVCA 1073

RESULT 14

C64073
Ibs repressor homolog - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 20-Aug-1999
C:Accession: C64073
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
; D.M.; Brandon, R.C.; Fife, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: C64073
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-332 <TIGR>
A:Cross-references: GB:U32732; GB:L42023; NID:G1573480; PIDN:AAC22164.1; PID:G1573487; T
C:Superfamily: lac repressor

Query Match 22.1%; Score 50.5; DB 2; Length 332;
Best Local Similarity 53.8%; Pred. No. 31;
Matches 14; Conservative 3; Mismatches 8; Indels 1; Gaps 1;

QY 20 LQIQSLGLDIDSRPTAEVCA 45
Db 224 VLGIQSL-LTQSSRPTAEVCCSDTIA 248

RESULT 15

E70813
Hypothetical protein Rv0845 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: E70813
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: E70813
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-425 <COL>
A:Cross-references: GB:AL022004; GB:AL123456; NID:G3261550; PIDN:CAA17651.1; PID:G125398
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv0845

Query Match 22.1%; Score 50.5; DB 2; Length 425;
Best Local Similarity 35.0%; Pred. No. 40;
Matches 14; Conservative 8; Mismatches 17; Indels 1; Gaps 1;

QY 1 MNGFASLLRNQFLLVFLQLQSLGLDIDSRPTAEVCA 40
Db 120 LTGFQLSLDGTGIVPLLMILLPV-LVGLDVSTRAAVILA 158

Search completed: March 8, 2004, 12:16:19
Job time : 14.1586 secs

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CM protein - protein search, using sw model

Run on: March 8, 2004, 12:07:46 ; Search time 11.9559 Seconds
(without alignments)
198.629 Million cell updates/sec

Title: US-09-600-932-2_COPY_1_46
Perfect score: 228
Sequence: 1 MNGFASLLRNQFILLVFL.....GLDIDSRPTAEVCATHITSP 46

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgm2_6/ptodata/2/iaa/5B COMB.pcp.*
3: /cgm2_6/ptodata/2/iaa/6A COMB.pcp.*
4: /cgm2_6/ptodata/2/iaa/6B COMB.pcp.*
5: /cgm2_6/ptodata/2/iaa/PCUTUS COMB.pcp.*
6: /cgm2_6/ptodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57.5	25.2	249	4	US-09-489-039A-13124
2	52	22.8	65	3	US-08-905-223-453
3	52	22.8	123	3	US-08-938-548B-10
4	52	22.8	123	4	US-08-939-093A-10
5	52	22.8	123	4	US-08-211-823C-10
6	52	22.8	130	3	US-08-938-548B-6
7	52	22.8	130	4	US-08-939-093A-6
8	52	22.8	130	4	US-08-230-896C-1
9	52	22.8	130	4	US-08-230-896C-2
10	52	22.8	130	4	US-09-211-823C-6
11	52	22.8	162	4	US-08-663-600A-126
12	52	22.8	162	4	US-08-663-600A-220
13	52	22.8	163	4	US-08-149-476-462
14	51.5	22.6	300	4	US-08-252-991A-27295
15	50	21.9	416	4	US-08-489-039A-13278
16	48.5	21.3	681	4	US-09-252-991A-18889
17	48	21.1	232	4	US-09-134-001C-4874
18	48	21.1	424	4	US-08-252-991A-18895
19	48	21.1	618	4	US-08-134-000C-6538
20	47.5	20.8	318	1	US-08-537-942A-1
21	47.5	20.8	318	3	US-08-997-252A-1
22	47.5	20.8	318	4	US-08-517-739-1
23	47.5	20.8	318	4	US-09-935-720A-1
24	47.5	20.8	362	4	US-09-485-648-6
25	47.5	20.8	362	4	US-09-503-565-6
26	47.5	20.8	362	4	US-08-485-649-6
27	47.5	20.8	423	4	US-09-252-991A-32616

28	47.5	20.8	718	4	US-09-252-991A-28229	Sequence 28229, A
29	47.5	20.8	1139	1	US-08-537-210A-4	Sequence 4, Appli
30	47.5	20.8	1139	3	US-09-113-825-4	Sequence 4, Appli
31	47.5	20.8	2703	1	US-08-185-432-19	Sequence 19, Appli
32	47.5	20.8	2703	4	US-08-899-232-4	Sequence 4, Appli
33	47	20.6	84	4	US-09-543-681A-7825	Sequence 7825, Ap
34	46.5	20.4	434	4	US-09-543-681A-6266	Sequence 6266, Ap
35	46.5	20.4	506	4	US-09-134-001C-4282	Sequence 4282, Ap
36	46.5	20.4	577	4	US-09-489-039A-12056	Sequence 12056, A
37	46	20.2	51	4	US-09-482-273-168	Sequence 168, App
38	46	20.2	81	4	US-09-482-273-262	Sequence 262, App
39	46	20.2	260	3	US-08-957-130-15	Sequence 15, Appl
40	46	20.2	277	4	US-09-252-991A-18435	Sequence 18435, A
41	46	20.2	281	3	US-08-808-148-4	Sequence 4, Appli
42	46	20.2	1044	4	US-09-252-991A-24495	Sequence 24495, A
43	45.5	20.0	197	4	US-09-252-991A-31560	Sequence 31560, A
44	45.5	20.0	445	4	US-09-134-001C-3507	Sequence 3507, Ap
45	45	19.7	69	4	US-09-107-532A-6826	Sequence 6826, Ap

ALIGNMENTS

RESULT 1
US-09-489-039A-13124
; Sequence 13124, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR FILING DATE: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13124
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13124

Query Match 25.2%; Score 57.5; DB 4; Length 249;
Best Local Similarity 35.9%; Pred. No. 0.6; 16; Indels 1; Gaps 1;
Matches 14; Conservative 8; Mismatches 16;

QY 4 FASLLRNQFILLVFL-LQIQLGLDIDSRPTAEVCAT 41
DB 88 YISLARATPLVTLVFLFLSLPTMGINKVAAIVALT 126

RESULT 2
US-08-905-223-453
; Sequence 453, Application US/08905223
; Patent No. 622029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duclert, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
; NUMBER OF SEQUENCES: 503
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martena, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95

;; SOFTWARE: Word
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/905,223
;; FILING DATE:
;; CLASSIFICATION: 536
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Israel, Ned A.
;; REGISTRATION NUMBER: 29,655
;; REFERENCE/DOCKET NUMBER:
;; TELEPHONE: (619) 235-8550
;; TELEFAX: (619) 235-0176
;; INFORMATION FOR SEQ ID NO: 453:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 65 amino acids
;; TYPE: AMINO ACID
;; TOPOLOGY: LINEAR
;; MOLECULE TYPE: PROTEIN
;; ORIGINAL SOURCE:
;; ORGANISM: Homo Sapiens
;; TISSUE TYPE: Brain
;; FEATURE:
;; NAME/KEY: sig_peptide
;; LOCATION: -21...-1
;; IDENTIFICATION METHOD: Von Heijne matrix
;; OTHER INFORMATION: score 5.6
;; OTHER INFORMATION: seq LVLSQLFLLSYD/LF
US-08-905-223-453

Query Match 22.8%; Score 52; DB 3; Length 65;
Best Local Similarity 45.5%; Pred. No. 0.77;
Matches 10; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 MNGFASLLRNQFILLVFLFIQ 22
Db 24 VNSFSELIQKTPVQLVFLFIQ 45

RESULT 3
US-08-938-548B-10
; Sequence 10, Application US/08938548B
; Patent No. 6001963
; GENERAL INFORMATION:
; APPLICANT: Yanagisawa, Masaashi
; APPLICANT: Bergsma, Derk
; APPLICANT: Wilson, Shelagh
; APPLICANT: Brooks, David
; APPLICANT: Gellai, Miklos
; TITLE OF INVENTION: NOVEL LIGANDS OF THE NEUROPEPTIDE
; TITLE OF INVENTION: RECEPTOR HFGAN72
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: United States of America
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,548B
; FILING DATE: 26-SEPT-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/887,382
; FILING DATE: 2-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/820,519
; FILING DATE: 19-MAR-1997

;; APPLICATION NUMBER: 60/033,604
;; FILING DATE: 17-DEC-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Elizabeth J. Hecht
;; REGISTRATION NUMBER: 41,824
;; REFERENCE/DOCKET NUMBER: ATG50037-2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 610-270-5009
;; TELEFAX: 610-270-5090
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 123 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-938-548B-10
Query Match 22.8%; Score 52; DB 3; Length 123;
Best Local Similarity 38.7%; Pred. No. 1.8;
Matches 12; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 15 LVVFLFIQISGLDIDSRPTAEVCATHIS 45
Db 8 LLLLLLPPALLSLGVDAQLPDCRQKICS 38

RESULT 4
US-08-939-093A-10
; Sequence 10, Application US/08939093A
; Patent No. 630854
; GENERAL INFORMATION:
; APPLICANT: Yanagisawa, Masaashi
; APPLICANT: Bergsma, Derk
; APPLICANT: Wilson, Shelagh
; APPLICANT: Brooks, David
; APPLICANT: Gellai, Miklos
; TITLE OF INVENTION: NOVEL LIGANDS OF THE NEUROPEPTIDE
; TITLE OF INVENTION: RECEPTOR HFGAN72
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: United States of America
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,093A
; FILING DATE: 26-SEPT-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/887,382
; FILING DATE: 2-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/820,519
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: 60/033,604
; FILING DATE: 17-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T.
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: ATG50037-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-4026
; TELEX:

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-939-093A-10

Query Match 22.8%; Score 52; DB 4; Length 123;
Best Local Similarity 38.7%; Pred. No. 1.8;
Matches 12; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 15 LVLFLQLQISGLGIDSRPTAEVCATHIS 45
DB 8 LLLLLLPPALLSLGVDAQPLDCCRCQKTC 38

RESULT 5

US-09-211-823C-10
Sequence 10, Application US/09211823C
Patent No. 6664229

GENERAL INFORMATION:
APPLICANT: HAGEN, JAMES JOSEPH
APPLICANT: TERRETT, JONATHAN ALEXANDER
APPLICANT: UPTON, NEIL
APPLICANT: PIPER, DAVID
APPLICANT: SMITH, MARTIN IAN
APPLICANT: KENNETH, GUY ANTHONY
APPLICANT: PATEL, SARASWATI R.

TITLE OF INVENTION: METHODS OF TREATMENT USING NOVEL LIGANDS
TITLE OF INVENTION: OF THE NEUROPEPTIDE RECEPTOR HFGAN72 AND AGONISTS OR
TITLE OF INVENTION: ANTAGONISTS THEREOF
FILE REFERENCE: P50745

CURRENT APPLICATION NUMBER: US/09/211,823C
CURRENT FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: US 60/069,459
PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 60/069,785
PRIOR FILING DATE: 1997-12-16

NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 10
LENGTH: 123
TYPE: PRT

ORGANISM: MUS MUSCULUS

US-09-211-823C-10

Query Match 22.8%; Score 52; DB 4; Length 123;
Best Local Similarity 38.7%; Pred. No. 1.8;
Matches 12; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 15 LVLFLQLQISGLGIDSRPTAEVCATHIS 45
DB 8 LLLLLLPPALLSLGVDAQPLDCCRCQKTC 38

RESULT 6

US-08-938-548B-6
Sequence 6, Application US/08938548B
Patent No. 6001963

GENERAL INFORMATION:
APPLICANT: Yanagisawa, Masashi
APPLICANT: Bergsma, Derk
APPLICANT: Wilson, Shelagh
APPLICANT: Brooks, David
APPLICANT: Gellai, Miklos

TITLE OF INVENTION: NOVEL LIGANDS OF THE NEUROPEPTIDE
TITLE OF INVENTION: RECEPTOR HFGAN72
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road

CITY: King of Prussia
STATE: PA
COUNTRY: United States of America
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,548B
FILING DATE: 26-SEPT-1997
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/887,382
FILING DATE: 2-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/820,519
FILING DATE: 19-MAR-1997

APPLICATION NUMBER: 60/033,604
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth J. Hecht
REGISTRATION NUMBER: 41,824
REFERENCE/DOCKET NUMBER: ATGS0037-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5009
TELEFAX: 610-270-5090

TELEX:

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-938-548B-6

Query Match 22.8%; Score 52; DB 3; Length 130;
Best Local Similarity 38.7%; Pred. No. 1.9;
Matches 12; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 15 LVLFLQLQISGLGIDSRPTAEVCATHIS 45
DB 15 LLLLLLPPALLSLGVDAQPLDCCRCQKTC 45

RESULT 7

US-08-939-093A-6
Sequence 6, Application US/08939093A
Patent No. 6309554

GENERAL INFORMATION:
APPLICANT: Yanagisawa, Masashi
APPLICANT: Bergsma, Derk
APPLICANT: Wilson, Shelagh
APPLICANT: Brooks, David
APPLICANT: Gellai, Miklos

TITLE OF INVENTION: NOVEL LIGANDS OF THE NEUROPEPTIDE
TITLE OF INVENTION: RECEPTOR HFGAN72
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: United States of America
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:

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/ APPLICATION NUMBER: US/08/939,093A
/ FILING DATE: 26-SEPT-1997
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/887,382
/ FILING DATE: 2-JUN-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/820,519
/ FILING DATE: 19-MAR-1997
/ APPLICATION NUMBER: 60/033,604
/ FILING DATE: 17-DEC-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: King, William T.
/ REGISTRATION NUMBER: 30,954
/ REFERENCE/DOCKET NUMBER: ATG50037-3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 610-270-5219
/ TELEFAX: 610-270-4026
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 130 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-939-093A-6

```

Query Match	22.8%;	Score 52;	DB 4;	Length 130;
Best Local Similarity	38.7%;	Pred. No. 1.9;		
Matches	12.	Conservative	5;	Mismatches 14;
		Indels	0;	Gaps 0;

QY 15 LVLFLQLQSLGLDIDSRPTAEVCATHTIS 45
||: || | | : : : | | |
pb 15 LLLLLPALLSLGVDAOPLPDCCKTCS 45

```

RESULT 8
US-09-230-896C-1
; Sequence 1, Application US/09230896C
; Patent No. 6635479
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Sutcliffe, et al.
; TITLE OF INVENTION: Hypothalamus-Specific Polypeptides
; FILE REFERENCE: TSI-548.1
; CURRENT APPLICATION NUMBER: US/09/230,896C
; CURRENT PILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: 60/023,220
; PRIOR PILING DATE: 1996-08-02
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 130
; TYPE: PRT
; ORGANISM: rat
; US-09-230-896C-1

```

Query Match 22.8%; Score 52; DB 4; Length 130;
Best Local Similarity 38.7%; Pred. No. 1.9;
Matches 12; Conservative 5; Mismatches 14; Indels

Qy 15 LVLFLQLQISGLDIDSRPTAEVCATHTIS 45
||: || | | : : | |
Db 15 LLLLLPPALLSLGVDAOPLDCCROKTCs 45

RESULT 9
US-09-230-896C-2
; Sequence 2, Application US/09230896C
; Patent No. 6635479
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute

```

; APPLICANT: Sutcliffe, et al.
; TITLE OF INVENTION: Hypothalamus-Specific Polypeptides
; FILE REFERENCE: TSRI-548.1
; CURRENT APPLICATION NUMBER: US/09/230,896C
; CURRENT FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: 60/023,220
; PRIOR FILING DATE: 1996-08-02
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 130
; TYPE: PRT
; ORGANISM: mus musculus
; PS-09-230-896C-2

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Query Match 22.8%; Score 52; DB 4; Length 130;
Best Local Similarity 38.7%; Pred. No. 1.9;
Matches 12: Conservative 5; Mismatches 14; Indels

QY 15 LLVLFILQIQSLGLDIDSRPTAEVCATHTIS 45
|||:|||::|:
db 15 LLLILLPPALLSLGVDAOPLPDCROKTCIS 45

```

RESULT 10
US-09-211-823C-6
Sequence 6, Application US/09211823C
Patent No. 6664229
GENERAL INFORMATION:
APPLICANT: HAGEN, JAMES JOSEPH
APPLICANT: TERRETT, JONATHAN ALEXANDER
APPLICANT: UPTON, NEIL
APPLICANT: PIPER, DAVID
APPLICANT: SMITH, MARTIN IAN
APPLICANT: KENNETH, GUY ANTHONY
APPLICANT: PATEL, SARASWATI R.
TITLE OF INVENTION: METHODS OF TREATMENT USING NOVEL LIGANDS
TITLE OF INVENTION: OF THE NEUROPEPTIDE RECEPTOR HFGAN72 AND AGONISTS OR
TITLE OF INVENTION: ANTAGONISTS THEREOF
FILE REFERENCE: P50745
CURRENT APPLICATION NUMBER: US/09/211,823C
CURRENT FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: US 60/069,459
PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 60/069,785
PRIOR FILING DATE: 1997-12-16
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 130
TYPE: PRT
ORGANISM: RATTUS RATTUS
US-09-211-823C-6

```

Query Match 22.8%; Score 52; DB 4; Length 130;
Best Local Similarity 38.7%; Pred. No. 1.9;
Matches 12; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

Qy 15 LLVFLFLQISGLDIDSRPTAEVCATHTIS 45
||: || | | | : | | | |
nb 15 LLLLLLPPALLSLGVDAOPLDCCFKTCS 45

RESULT 11
US-09-663-600A-126
; Sequence 126, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Wilne Edwards, Jean-Baptiste
; APPLICANT: Duciert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP

Query Match 22.8%; Score 52; DB 4; Length 162;
Best Local Similarity 45.5%; Pred. No. 2.5;
Matches 10; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 MNGFASILLRNQFILLVLFLLQ 22
DB 24 VNSFSELLQKTPVQLVLFIIQ 45

RESULT 13
US-09-149-476-462
; Sequence 462, Application US/09149476
; Patent No. 8420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23

Query Match 22.8%; Score 52; DB 4; Length 162;
Best Local Similarity 45.5%; Pred. No. 2.5;
Matches 10; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 MNGFASILLRNQFILLVLFLLQ 22
DB 24 VNSFSELLQKTPVQLVLFIIQ 45

RESULT 12
US-09-663-600A-220
; Sequence 220, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CTP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; EARLIER APPLICATION NUMBER: 09/191,997
; EARLIER FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: 60/066,677
; EARLIER FILING DATE: 1997-11-13
; EARLIER APPLICATION NUMBER: 60/069,957
; EARLIER FILING DATE: 1997-12-17
; EARLIER APPLICATION NUMBER: 60/074,121
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/081,563
; EARLIER FILING DATE: 1998-04-13
; EARLIER APPLICATION NUMBER: 60/096,116
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/099,273
; EARLIER FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 126
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -21...-1
; US-09-663-600A-126

QY 1 MNGFASILLRNQFILLVLFLLQ 22
DB 24 VNSFSELLQKTPVQLVLFIIQ 45

US-09-663-600A-220

EARLIER APPLICATION NUMBER: 60/047,612
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,632
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,601
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,580
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,568
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,314
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,569
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,311
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,671
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,674
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,669
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,312
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,313
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,672
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,315
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,877
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,889
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,893
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,630
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,878
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,662
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,872
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,882
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,637
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,903
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,888
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,879
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,880
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,894
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,911
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,636
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,874
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,910
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,864
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,631

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,845
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,892
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,761
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047,595
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,599
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,588
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,585
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,586
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,590
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,594
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,589
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,593
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,684
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 22.8%; Score 52; DB 4; Length 163;
Best Local Similarity 45.5%; Pred. No. 2.6;
Matches 10; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 MNGFASLRRNQFILLVLFLLQ 22
DB 24 VNSFSELLQKTFVLQVLFLLQ 45

RESULT 14
US-09-252-991A-27295
; Sequence 27295, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27295
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27295

Query Match 22.6%; Score 51.5; DB 4; Length 300;
Best Local Similarity 29.3%; Pred. NO. 6.7;
Matches 17; Conservative 7; Mismatches 15; Indels 19; Gaps 2;
QY 8 LRNQFILLVLFLLQI-----QSLG---LDIDSRPTAEVCATHITSP 46
DB 134 LQSMVALLVSLQCCRRPPPPRPSGRGQQLGAGEQLDVAADPATVCRDLDP 191

RESULT 15
US-09-489-039A-13278
; Sequence 13278, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13278
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13278

Query Match 21.9%; Score 50; DB 4; Length 416;
Best Local Similarity 34.3%; Pred. NO. 18;
Matches 12; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
QY 1 MNGFASLLRRNQFILLVLFLLQIQLGIDIDSRPT 35
DB 108 MDDYRRVRRLLILLALLIVASLLIDFMLGPS 142

Search completed: March 8, 2004, 12:17:26
Job time : 12.9559 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 11:54:00 ; Search time 42.3524 Seconds

(without alignments)
306.882 Million cell updates/sec

Title: US-09-600-932-2_COPY_1_46

Perfect score: 228
Sequence: 1 MNGFASLLRNQFILLVFL.....GLDIDSRPTAEVCATHITSP 46

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 29Jan04:*

- 1: geneseqp1980a:*
- 2: geneseqp1990a:*
- 3: geneseqp2000a:*
- 4: geneseqp2001a:*
- 5: geneseqp2002a:*
- 6: geneseqp2003a:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	228	100.0	277	2	AAY25518 Human col
2	228	100.0	277	2	AAY41698 Human PRO
3	228	100.0	277	3	AAB44254 Human PRO
4	228	100.0	277	4	AU29073 Human PRO
5	228	100.0	277	4	AU29073 Human PRO
6	228	100.0	277	6	ABU89977 Novel hum
7	228	100.0	277	6	ABU84312 Human sec
8	228	100.0	277	6	ABR66186 Human sec
9	228	100.0	277	6	ABR65576 Human sec
10	228	100.0	277	6	ABU99516 Human sec
11	228	100.0	277	6	ABU82755 Human PRO
12	228	100.0	277	6	ABU89876 Novel hum
13	228	100.0	277	6	ABR68125 Human sec
14	228	100.0	277	6	ABU96178 Novel hum
15	228	100.0	277	6	ABU92609 Human sec
16	228	100.0	277	6	ABO08686 Human sec
17	228	100.0	277	6	ABO02738 Human sec
18	228	100.0	277	6	ABR74892 Human sec
19	228	100.0	277	6	ABR94654 Human sec
20	228	100.0	277	6	ABO25200 Novel hum
21	228	100.0	277	6	ABU85627 Novel hum
22	228	100.0	277	6	ABU98787 Novel hum
23	228	100.0	277	6	ABU98002 Novel hum
24	228	100.0	277	6	ABU91708 Novel hum
25	228	100.0	277	6	ABU72206 Novel hum

26	228	100.0	277	6	ABU89401 Human PRO
27	228	100.0	277	6	ABU86242 Human sec
28	228	100.0	277	6	ABU67455 Human PRO
29	228	100.0	277	6	ABU80483 Human PRO
30	228	100.0	277	6	ABR9401 Human sec
31	228	100.0	277	6	ABR98791 Human sec
32	228	100.0	277	6	ABO16314 Human sec
33	228	100.0	277	6	ABR92214 Human sec
34	228	100.0	277	6	ABO18855 Human sec
35	228	100.0	277	6	ABR78276 Human sec
36	228	100.0	277	6	ABU85012 Novel hum
37	228	100.0	277	6	ABO00151 Novel hum
38	228	100.0	277	6	ABO11483 Human sec
39	228	100.0	277	6	ABO02128 Human sec
40	228	100.0	277	6	ABU88702 Human sec
41	228	100.0	277	6	ABU83397 Human sec
42	228	100.0	277	6	ABO06198 Novel hum
43	228	100.0	277	6	ABR59234 Human sec
44	228	100.0	277	6	ABO09296 Human sec
45	228	100.0	277	6	ABO19160 Novel hum

ALIGNMENTS

RESULT 1
AAY25518
ID AAY25518 standard; protein; 277 AA.

XX AC AAY25518;
XX 30-SEP-1999 (first entry)
XX Human collectin protein.
XX Collectin; human; antibacterial; antiviral; treatment; infection.
XX Homo sapiens.
XX WO9937767-A1.
XX 29-JUL-1999.
XX 24-JUL-1998; 98WO-JP003328.
XX 23-JAN-1998; 98JP-00011281.
XX (FUSO) FUSO PHARM IND LTD.
XX Wakamiya N;
XX WPI; 1999-458691/38.
XX N-PSDB; AAX88323.
XX New collectin protein of human origin and DNA encoding it.
XX Claim 1; Page 42-44; 58pp; Japanese.
XX This invention describes the isolation and characterisation of a novel human collectin protein and its encoding polynucleotide. The human collectin exhibits antibacterial and antiviral activity and can be used as an agent for the treatment of human bacterial and viral infections.
XX This sequence represents the novel human collectin
SQ Sequence 277 AA;

Query Match 100.0%; Score 228; DB 2; Length 277;
Best Local Similarity 100.0%; Pred. No. 4.4e-24;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGFASLLRNQFILLVFLFLLQSLGLDIDSRPTAEVCATHITSP 46
DB 1 MNGFASLLRNQFILLVFLFLLQSLGLDIDSRPTAEVCATHITSP 46

```
RESULT 2
AA41698
ID AAY41698 standard; protein; 277 AA.
AC
XX AAY41698;
DT 07-DEC-1999 (first entry)
XX
DE Human PRO702 protein sequence.
XX
KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein.
XX
OS Homo sapiens.
XX
XX WO9946281-A2.
XX
PD 16-SEP-1999.
XX
XX 08-MAR-1999; 99WO-US005028.
XX
XX 10-MAR-1998; 98US-0077450P.
XX 11-MAR-1998; 98US-0077632P.
XX 11-MAR-1998; 98US-0077641P.
XX 11-MAR-1998; 98US-0077649P.
XX 12-MAR-1998; 98US-0077791P.
XX 13-MAR-1998; 98US-0078004P.
XX 17-MAR-1998; 98US-0004022P.
XX 20-MAR-1998; 98US-0078886P.
XX 20-MAR-1998; 98US-0078910P.
XX 20-MAR-1998; 98US-0078936P.
XX 20-MAR-1998; 98US-0078939P.
XX 25-MAR-1998; 98US-0079294P.
XX 26-MAR-1998; 98US-0079656P.
XX 27-MAR-1998; 98US-0079663P.
XX 27-MAR-1998; 98US-0079664P.
XX 27-MAR-1998; 98US-0079689P.
XX 27-MAR-1998; 98US-0079728P.
XX 30-MAR-1998; 98US-0079920P.
XX 30-MAR-1998; 98US-0079923P.
XX 31-MAR-1998; 98US-0080103P.
XX 31-MAR-1998; 98US-0080107P.
XX 31-MAR-1998; 98US-0080165P.
XX 31-MAR-1998; 98US-0080194P.
XX 01-APR-1998; 98US-0080327P.
XX 01-APR-1998; 98US-0080328P.
XX 01-APR-1998; 98US-0080333P.
XX 01-APR-1998; 98US-0080334P.
XX 08-APR-1998; 98US-0081049P.
XX 08-APR-1998; 98US-0081070P.
XX 08-APR-1998; 98US-0081071P.
XX 09-APR-1998; 98US-0081195P.
XX 09-APR-1998; 98US-0081203P.
XX 09-APR-1998; 98US-0081229P.
XX 15-APR-1998; 98US-0081817P.
XX 15-APR-1998; 98US-0081838P.
XX 15-APR-1998; 98US-0081952P.
XX 15-APR-1998; 98US-0081955P.
XX 21-APR-1998; 98US-0082568P.
XX 21-APR-1998; 98US-0082569P.
XX 22-APR-1998; 98US-0082700P.
XX 22-APR-1998; 98US-0082704P.
XX 22-APR-1998; 98US-0082804P.
XX 23-APR-1998; 98US-0082767P.
XX 23-APR-1998; 98US-0082796P.
XX 27-APR-1998; 98US-0083336P.
XX 28-APR-1998; 98US-0083322P.
XX 29-APR-1998; 98US-0083392P.
XX 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083500P.
PR 29-APR-1998; 98US-0083545P.
PR 29-APR-1998; 98US-0083554P.
PR 29-APR-1998; 98US-0083558P.
PR 29-APR-1998; 98US-0083559P.
PR 30-APR-1998; 98US-0083742P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 06-MAY-1998; 98US-0084441P.
PR 07-MAY-1998; 98US-0084598P.
PR 07-MAY-1998; 98US-0084600P.
PR 07-MAY-1998; 98US-0084627P.
PR 07-MAY-1998; 98US-0084637P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084840P.
PR 07-MAY-1998; 98US-0084843P.
PR 13-MAY-1998; 98US-0085323P.
PR 13-MAY-1998; 98US-0085338P.
PR 13-MAY-1998; 98US-0085339P.
PR 15-MAY-1998; 98US-0085573P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085800P.
PR 15-MAY-1998; 98US-0085862P.
PR 15-MAY-1998; 98US-0085869P.
PR 15-MAY-1998; 98US-0085697P.
PR 15-MAY-1998; 98US-0085700P.
PR 15-MAY-1998; 98US-0085704P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Wood WJ, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
PI
XX WPI, 1999-551358/46.
XX N-PSDB; AAZ33973.
XX
XX New secreted and transmembrane polypeptides and their polynucleotides,
XX useful for treating blood coagulation disorders, cancers and cellular
XX adhesion disorders.
XX
XX Claim 12; Fig 37; 530pp; English.
XX
XX The present invention describes secreted and transmembrane polypeptides
XX and their polynucleotides. The nucleotide sequences are useful as sources
XX of probes, primers, for chromosome mapping, and for generation of
XX antisense sequences. They can also be used to create transgenic animals.
XX The proteins can be used to treat a variety of diseases and disorders,
XX depending on their function. Diseases that may be treated include blood
XX coagulation disorders, cancers and cellular adhesion disorders. They may
XX also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to
XX AAY41774 represent polynucleotide and polypeptide sequence given in the
XX exemplification of the present invention
XX
XX Sequence 277 AA;
XX
XX Query Match 100.0%; Score 228; DB 2; Length 277;
XX Best Local Similarity 100.0%; Pred. No. 4.4e-24;
XX Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MNGFASLLRRNQFILLVFLVLIQSLGLDIDSRPTAEVCATHHTISP 46
XX 1 MNGFASLLRRNQFILLVFLVLIQSLGLDIDSRPTAEVCATHHTISP 46
XX
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RESULT 3

AAB44254

ID AAB44254 standard; protein; 277 AA.

XX AAB44254;

AC AAB44254;

XX

DT 08-FEB-2001 (first entry)

XX

DE Human PRO702 (UNQ366) protein sequence SEQ ID NO:97.

KW Human; secreted protein; transmembrane protein; PRO; EST; cytosstatic;

KW expressed sequence tag; detection; cancer.

XX

JS Homo sapiens.

XX

FN WO200053756-A2.

XX

PD 14-SEP-2000.

XX

PF 18-FEB-2000; 2000WO-US004341.

XX

PR 08-MAR-1999; 99WO-US005028.

PR

PR 12-MAR-1999; 99US-0123957P.

PR

PR 29-MAR-1999; 99US-0126773P.

PR

PR 21-APR-1999; 99US-0130232P.

PR

PR 28-APR-1999; 99US-0131445P.

PR

PR 14-MAY-1999; 99US-0134287P.

PR

PR 23-JUN-1999; 99US-0141037P.

PR

PR 29-OCT-1999; 99US-0145698P.

PR

PR 02-DEC-1999; 99WO-US028313.

PR

PR 02-DEC-1999; 99WO-US028551.

PR

PR 16-DEC-1999; 99WO-US030035.

PR

PR 30-DEC-1999; 99WO-US031243.

PR

PR 05-DEC-1999; 99WO-US031274.

PR

PR 05-JAN-2000; 2000WO-US000219.

PR

PR 06-JAN-2000; 2000WO-US000277.

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PR 06-JAN-2000; 2000WO-US000376.

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(GETH) GENENTECH INC.

Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;

Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;

Goddard A, Godowski PJ, Grimaldi CU, Gurney AL, Hillan KJ;

Klavin IJ, Kuo SS, Napier MA, Pan J, Paoni NP, Roy MA, Shelton DL;

Stewart TA, Tumas D, Williams PM, Wood WI;

WPI; 2000-611443/58.

N-PSDB; AAC78480.

Novel PRO polypeptides and polynucleotides used in detection methods, to

target bioactive molecules to specific cells, and to modulate cellular

activities.

Claim 12; Fig 37; 636pp; English.

AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence

tag) sequences which encode secreted or transmembrane PRO polypeptides.

The PRO polynucleotides and polypeptides have cytosstatic activity. The

polynucleotides and polypeptides can be used for detecting the presence

of PRO polypeptides in samples, for linking bioactive molecules to cells

and for modulating biological activities of cells, using the polypeptides

for specific targeting. The polypeptide targeting can be used to kill the

target cells, e.g. for the treatment of cancers. The polypeptide pairs

provide specific targeting of bioactive molecules to cells. AAC78600 to

AAC78987 represent PCR primers and probes used in the isolation of the

PRO polynucleotide sequences

Sequence 277 AA;

Sequence 277 AA;

Sequence 277 AA;

Sequence 277 AA;

Sequence 277 AA;

Sequence 277 AA;

Sequence 277 AA;

Sequence 277 AA;

Sequence 277 AA;

Sequence 277 AA;

Sequence 277 AA;

Sequence 277 AA;

Sequence 277 AA;

Sequence 277 AA;

Sequence 277 AA;

Sequence 277 AA;

Sequence 277 AA;

Query Match 100.0%; Score 228; DB 3; Length 277;

Best Local Similarity 100.0%; Pred. NO. 4.4e-24;

Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MNGFASLLRRNQIFLLVLFLLQISLGLDIDSRPTAEVCATHTISP 46

1 MNGFASLLRRNQIFLLVLFLLQISLGLDIDSRPTAEVCATHTISP 46

1 MNGFASLLRRNQIFLLVLFLLQISLGLDIDSRPTAEVCATHTISP 46

1 MNGFASLLRRNQIFLLVLFLLQISLGLDIDSRPTAEVCATHTISP 46

1 MNGFASLLRRNQIFLLVLFLLQISLGLDIDSRPTAEVCATHTISP 46

1 MNGFASLLRRNQIFLLVLFLLQISLGLDIDSRPTAEVCATHTISP 46

1 MNGFASLLRRNQIFLLVLFLLQISLGLDIDSRPTAEVCATHTISP 46

1 MNGFASLLRRNQIFLLVLFLLQISLGLDIDSRPTAEVCATHTISP 46

1 MNGFASLLRRNQIFLLVLFLLQISLGLDIDSRPTAEVCATHTISP 46

1 MNGFASLLRRNQIFLLVLFLLQISLGLDIDSRPTAEVCATHTISP 46

1 MNGFASLLRRNQIFLLVLFLLQISLGLDIDSRPTAEVCATHTISP 46

1 MNGFASLLRRNQIFLLVLFLLQISLGLDIDSRPTAEVCATHTISP 46

1 MNGFASLLRRNQIFLLVLFLLQISLGLDIDSRPTAEVCATHTISP 46

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1 MNGFASLLRRNQIFLLVLFLLQISLGLDIDSRPTAEVCATHTISP 46

1 MNGFASLLRRNQIFLLVLFLLQISLGLDIDSRPTAEVCATHTISP 46

1 MNGFASLLRRNQIFLLVLFLLQISLGLDIDSRPTAEVCATHTISP 46

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1 MNGFASLLRRNQIFLLVLFLLQISLGLDIDSRPTAEVCATHTISP 46

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1 MNGFASLLRRNQIFLLVLFLLQISLGLDIDSRPTAEVCATHTISP 46

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1 MNGFASLLRRNQIFLLVLFLLQISLGLDIDSRPTAEVCATHTISP 46

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1 MNGFASLLRRNQIFLLVLFLLQISLGLDIDSRPTAEVCATHTISP 46

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XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2001-602746/68.
 DR N-PSDB; AAS45974.
 XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 PT presence of tumors, such as prostate and breast tumors, in mammals and to
 PT screen for modulators of the compounds.
 XX Claim 11; Fig 100; 774pp; English.
 XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
 CC The PRO polypeptides and their associated nucleic acids can be used to
 CC detect the presence of a tumour in a mammal by comparing the level of
 CC expression of a PRO polypeptide in a test sample of cells from the animal
 CC and a control sample of normal cells, whereby a higher level of
 CC expression in the test sample indicates the presence of a tumour in the
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
 CC and rabbits but are preferably human. The polypeptides can be used to
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
 CC when contacted with it. A specific polypeptide can be used to stimulate
 CC the proliferation or differentiation of chondrocyte cells. The PRO
 CC proteins can be used to determine the presence of tumours and also
 CC susceptibility to tumour development, particularly adrenal, lung, colon,
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
 CC can be used for genetic analysis of individuals with genetic disorders
 XX Sequence 277 AA;
 SQ

Query Match 100.0%; Score 228; DB 4; Length 277;
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RESULT 5
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 XX OS Homo sapiens.
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 XX PF 21-JUN-2002; 2002US-00176492.
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RESULT 7
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XX AC ABU84312;
XX DT 02-AUG-2003 (first entry)
XX DE Human secreted/transmembrane protein (PRO) #50.
XX KW Human; secreted and transmembrane protein; PRO; TNF-alpha;
XX KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
XX OS Homo sapiens.
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XX PD 13-FEB-2003.
XX PF 21-JUN-2002; 2002US-00176756.
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RESULT 8
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ID ABR66186 standard; protein; 277 AA.
XX AC ABR66186;
XX DT 05-AUG-2003 (first entry)
XX DE Human secreted polypeptide PRO702, SEQ ID NO:100.
XX KW Human; PRO; secreted protein; transmembrane protein; TNF-alpha;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnerary; gene therapy.
XX OS Homo sapiens.
XX FN US2003027278-A1.
XX PD 06-FEB-2003.
XX PF 21-JUN-2002; 2002US-00176987.
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Best Local Similarity 100.0%; Pred. No. 4.4e-24;
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Db 1 MNGFASLLRRNQFILLVFLQLQISLGLDIDSRPTAEVCATHTISP 46

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ID ABR65576 standard; protein; 277 AA.
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AC ABR65576;
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DT 05-AUG-2003 (first entry)
XX
DE Human secreted polypeptide PRO702, SEQ ID NO:100.
XX
KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antarthritic; vulnery; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003036159-A1.
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PD 20-FEB-2003.
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PF 02-JUL-2002; 2002US-00188773.
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Query Match 100.0%; Score 228; DB 6; Length 277;
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XX AC ABU99516;

XX DT 09-AUG-2003 (first entry)

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XX Human; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
tissue typing.

XX OS Homo sapiens.

XX PN US2003040070-A1.

XX PD 27-FEB-2003.

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KX antiarthritic; vulnery; gene therapy.
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XX DT 25-JUL-2003 (first entry)
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XX QY 01-JUL-2002; 2002US-00187601.
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ALIGNMENTS

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- APPLICANT: Ashkenazi, Avi
- APPLICANT: Baker Kevin P.
- APPLICANT: Botstein, David
- APPLICANT: Desnovers, Luc
- APPLICANT: Eaton, Dan
- APPLICANT: Ferrara, Napoleon
- APPLICANT: Filvaroff, Ellen
- APPLICANT: Fong, Sherman
- APPLICANT: Gao, Wei-Qiang
- APPLICANT: Gerber, Hanspeter
- APPLICANT: Gerritsen, Mary E.
- APPLICANT: Goddard, Audrey
- APPLICANT: Godowski, Paul J.
- APPLICANT: Grimaldi, J. Christopher
- APPLICANT: Gurney, Austin L.
- APPLICANT: Hillan, Kenneth J.
- APPLICANT: Kijavini, Ivar J.
- APPLICANT: Kuo, Sophia S.
- APPLICANT: Napier, Mary A.
- APPLICANT: Paoni, Nicholas F.
- APPLICANT: Roy, Margaret Ann
- APPLICANT: Sheiton, David L.
- APPLICANT: Stewart, Timothy A.
- APPLICANT: Tumas, Daniel
- APPLICANT: Williams, P. Mickey
- APPLICANT: Wood, William I.
- TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
- TITLE OF INVENTION: Acids Encoding the Same
- FILE REFERENCE: P2630P1C11
- CURRENT APPLICATION NUMBER: US/09/978, 295A
- CURRENT FILING DATE: 2001-10-15
- PRIOR APPLICATION NUMBER: 09/918585

PRIOR APPLICATION NUMBER: 60/081222	PRIOR FILING DATE: 1998-04-09
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US-09-978-697-97
Sequence 97, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P26301C27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.0%; Score 390; DB 9; Length 277;
Best Local Similarity 98.6%; Pred. No. 5.8e-34;
Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 47 GPKGDDGEGKDPGEKGKGVGRMGPKGIKGLGDMGRGNIGKTGPIGKKGDKGEGKGLL 106
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QY 61 GIPGEGKAGTV 72
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Db 107 GIPGEGKAGTV 118
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RESULT 3

US-09-978-192A-97
; Sequence 97, Application US/09978192A
; Patent No. US20020177553A1

GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Baker Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleon
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Kuo, Sophia S.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR APPLICATION NUMBER: 60/065311

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9 PRIOR FILING DATE: 1998-05-15
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12 PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.0%; Score 390; DB 9; Length 277;
Best Local Similarity 98.6%; Pred. No. 5.8e-34;
Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 61 GIPGKKGKAGTV 72
DB 107 GIPGKKGKAGTV 118

RESULT 4
US-09-999-832A-97
Sequence 97, Application US/09999832A
Publication No. US20020192706A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desrochers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Fan, James
APPLICANT: Faoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC63
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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/ PRIOR APPLICATION NUMBER: 60/085697

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Qy 61 GIPGEKGKAGTV 72
Db 107 GIPGEKGKAGTV 118

RESULT 5
US-09-978-189-97
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/ Publication No. US20030004102A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnovers, Luc
/ APPLICANT: Eaton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Justin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kljavin, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ TITLE OF INVENTION: Acids Encoding the Same
/ FILE REFERENCE: P2630P1C7
/ CURRENT APPLICATION NUMBER: US/09/978,189
/ CURRENT FILING DATE: 2001-10-15
/ PRIOR APPLICATION NUMBER: 09/918585
/ PRIOR FILING DATE: 2001-07-30
/ PRIOR APPLICATION NUMBER: 60/062250
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/064249
/ PRIOR FILING DATE: 1997-11-03
/ PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match
Best Local Similarity 99.0%; Score 390; DB 10; Length 277;
Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 47 GPKGDDGKGPGEKGKGVGRMGPKIGKELGMDGDRNIGKTGPIGKKGDKGKGLL 106

2Y 61 GIPGEKKGAGTV 72
Db 107 GIPGEKKGAGTV 118

RESULT 6
US-09-978-608A-97
; Sequence 97, Application US/09978608A
; Publication No. US2003004562A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 97
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-97

Query Match
Best Local Similarity 99.0%; Score 390; DB 10; Length 277;
Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

2Y 1 GPKGDDGKGPGEKGKGVGRMGPKIGKELGMDGDRNIGKTGPIGKKGDKGKGLL 60
Db 47 GPKGDDGKGPGEKGKGVGRMGPKIGKELGMDGDRNIGKTGPIGKKGDKGKGLL 106

2Y 61 GIPGEKKGAGTV 72
Db 107 GIPGEKKGAGTV 118

RESULT 7
US-09-978-585A-97
; Sequence 97, Application US/09978585A
; Publication No. US2003004963A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 97
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585A-97

Query Match
Best Local Similarity 99.0%; Score 390; DB 10; Length 277;
Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

2Y 1 GPKGDDGKGPGEKGKGVGRMGPKIGKELGMDGDRNIGKTGPIGKKGDKGKGLL 60
Db 47 GPKGDDGKGPGEKGKGVGRMGPKIGKELGMDGDRNIGKTGPIGKKGDKGKGLL 106

2Y 61 GIPGEKKGAGTV 72
Db 107 GIPGEKKGAGTV 118

RESULT 8
US-09-978-191A-97
; Sequence 97, Application US/09978191A
; Publication No. US2003005023A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 97
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-97

Query Match
Best Local Similarity 99.0%; Score 390; DB 10; Length 277;
Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

2Y 1 GPKGDDGKGPGEKGKGVGRMGPKIGKELGMDGDRNIGKTGPIGKKGDKGKGLL 60
Db 47 GPKGDDGKGPGEKGKGVGRMGPKIGKELGMDGDRNIGKTGPIGKKGDKGKGLL 106
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Qy 61 GIPGEKKGAGTV 72
Db 107 GIPGEKKGAGTV 118

RESULT 7
US-09-978-585A-97
; Sequence 97, Application US/09978585A
; Publication No. US2003004963A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 97
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585A-97

Query Match
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Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPKGDDGKGPGEKGKGVGRMGPKIGKELGMDGDRNIGKTGPIGKKGDKGKGLL 60
Db 47 GPKGDDGKGPGEKGKGVGRMGPKIGKELGMDGDRNIGKTGPIGKKGDKGKGLL 106

Qy 61 GIPGEKKGAGTV 72
Db 107 GIPGEKKGAGTV 118

RESULT 8
US-09-978-191A-97
; Sequence 97, Application US/09978191A
; Publication No. US2003005023A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 97
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585A-97

Query Match
Best Local Similarity 99.0%; Score 390; DB 10; Length 277;
Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPKGDDGKGPGEKGKGVGRMGPKIGKELGMDGDRNIGKTGPIGKKGDKGKGLL 60
Db 47 GPKGDDGKGPGEKGKGVGRMGPKIGKELGMDGDRNIGKTGPIGKKGDKGKGLL 106

Qy 61 GIPGEKKGAGTV 72
Db 107 GIPGEKKGAGTV 118
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APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Eilen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Giang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kllavin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2630P1C4
 CURRENT APPLICATION NUMBER: US/09/978,191A
 CURRENT FILING DATE: 2001-10-15
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
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 PRIOR FILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/079923
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 PRIOR FILING DATE: 1998-03-31
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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.0%; Score 390; DB 10; Length 277;

Best Local Similarity 98.6%; Pred. No. 5.8e-34;

Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGDDGKGGPGEKKGKGYRMPKGIKGLGDMGDRNGTGTGPIGKKGDKGKGLL 60

Db 47 GPKGDDGKGGPGEKKGKGYRMPKGIKGLGDMGDRNGTGTGPIGKKGDKGKGLL 106

QY 61 GIPGKKGKAGTV 72

Db 107 GIPGKKGKAGTV 118

RESULT 9

US-09-978-403A-97

Sequence 97, Application US/09978403A

Publication No. US2003005240A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Kijavini, Ivar J.
;; APPLICANT: Kuo, Sophia S.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tunas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: P2630P1C17
;; CURRENT APPLICATION NUMBER: US/09/978,403A
;; CURRENT FILING DATE: 2002-03-19
;; PRIOR APPLICATION NUMBER: 09/918585
;; PRIOR FILING DATE: 2001-07-30
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;; PRIOR APPLICATION NUMBER: 60/083559
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083500
;; PRIOR FILING DATE: 1998-04-29

;; PRIOR APPLICATION NUMBER: 60/083742
;; PRIOR FILING DATE: 1998-04-30
;; PRIOR APPLICATION NUMBER: 60/084366
;; PRIOR FILING DATE: 1998-05-05
;; PRIOR APPLICATION NUMBER: 60/084414
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;; PRIOR APPLICATION NUMBER: 60/084637
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;; PRIOR FILING DATE: 1998-05-13
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;; PRIOR FILING DATE: 1998-05-15
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.0%; Score 390; DB 10; Length 277;

Best Local Similarity 98.6%; Pred. No. 5.8e-34; Mismatches 0; Indels 0; Gaps 0;
Matches 71; Conservative 1;

QY 1 GPKGDDGEGKDPGEEGKHGKVGKMGPKGKIGKELGDMGDRGNIGKTGPIKKGDKGKKGILL 60
Db 47 GPKGDDGEGKDPGEEGKHGKVGKMGPKGKIGKELGDMGDRGNIGKTGPIKKGDKGKKGILL 106

QY 61 GIPGEGKAGTV 72
Db 107 GIPGEGKAGTV 118

RESULT 10
US-09-978-564A-97
; Sequence 97, Application US/09978564A
; Publication No. US20030050241A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C25
CURRENT APPLICATION NUMBER: US/09/978,564A
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
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PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
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PRIOR APPLICATION NUMBER: 60/078939
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PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
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PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31

PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
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PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
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;; PRIOR FILING DATE: 1998-05-05
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;; PRIOR APPLICATION NUMBER: 60/084637
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;; PRIOR FILING DATE: 1998-05-15
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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.0%; Score 390; DB 10; Length 277;
Best Local Similarity 98.6%; Pred. No. 5.8e-34;
Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGDDGKGDGEGKKGKGVGRGPKGKIGELGDMGDRGNIGKTGPIGKKGDKGKGLL 60
DB 47 GPKGDDGKGDGEGKKGKGVGRGPKGKIGELGDMGDRGNIGKTGPIGKKGDKGKGLL 106

QY 61 GIPGKKGKAGTV 72
DB 107 GIPGKKGKAGTV 118

RESULT 11
US-09-999-833A-97
; Sequence 97, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher

;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Kuo, Sophia S.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2630P1065
;; CURRENT APPLICATION NUMBER: US/09/999,833A
;; CURRENT FILING DATE: 2001-10-24
;; PRIOR APPLICATION NUMBER: 09/918585
;; PRIOR FILING DATE: 2001-07-30
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;; PRIOR FILING DATE: 1997-10-17
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;; PRIOR APPLICATION NUMBER: 60/080194

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; PRIOR FILING DATE: 1998-04-29
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; PRIOR APPLICATION NUMBER: 60/084441
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; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.0%; Score 390; DB 10; Length 277;

Best Local Similarity 98.6%; Pred. No. 5.8e-34;

Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGDDGKGDGFGGKGGKGVGMGPKIKGELGDMGDRGNIGKTGPIGKKGDKGKGLL 60

Db 47 GPKGDDGKGDGFGGKGGKGVGMGPKIKGELGDMGDRGNIGKTGPIGKKGDKGKGLL 106

QY 61 GIPGKKGKAGTV 72

Db 107 GIPGKKGKAGTV 118

RESULT 12

US-09-981-915A-97

; Sequence 97, Application US/09981915A

; Publication No. US20030054986A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C12
CURRENT APPLICATION NUMBER: US/09/981,915A
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
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PRIOR FILING DATE: 1998-04-08
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PRIOR FILING DATE: 1998-04-08
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.0%; Score 390; DB 10; Length 277;

Best Local Similarity 98.6%; Pred. No. 5.8e-34;
Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPXGDDGKGDGPGEKGKGVGMGPKGKIGLGDMDRGNIGKTGPIGKKGKGEKGLL 60
DB 47 GPXGDDGKGDGPGEKGKGVGMGPKGKIGLGDMDRGNIGKTGPIGKKGKGEKGLL 106
QY 61 GIPGEGKAGTV 72
DB 107 GIPGEGKAGTV 118

RESULT 14

US-09-918-585A-97
; Sequence 97, Application US/09918585A
; Publication No. US20030060406A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C1
CURRENT APPLICATION NUMBER: US/09/918.585A
CURRENT FILING DATE: 2001-07-30
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Query Match 99.0%; Score 390; DB 10; Length 277;
Best Local Similarity 98.6%; Pred. No. 5.8e-34;
Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Db 47 GPKGDDGEKGDPEEGKHGKVGMPGKIGKBLGMDGDRNIGKTGPIGKKGDKGKGLL 106
Qy 61 GIPGEGKAGTV 72
Db 107 GIPGEGKAGTV 118

RESULT 15
US-09-978-423A-97
Sequence 97 Application US/09978423A
Publication No. US20030069178A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Flivaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pat, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2630P1C21
CURRENT APPLICATION NUMBER: US/09/978,423A
CURRENT FILING DATE: 2002-05-16
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; PRIOR FILING DATE: 1998-05-15

Query Match 99.0%; Score 390; DB 10; Length 277;
Best Local Similarity 98.6%; Pred. No. 5.8e-34;
Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGDDGKGDPEEGKHGKVGKMGPKGKIGKELGDMGDRGNIGKTGPIKKGDKGKGLL 60
Db 47 GPKGDDGKGDPEEGKHGKVGKMGPKGKIGKELGDMGDRGNIGKTGPIKKGDKGKGLL 106

QY 61 GIPGKKGKAGTV 72
Db 107 GIPGKKGKAGTV 118

Search completed: March 8, 2004, 12:18:56
Job time : 26.0088 secs

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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:02:31 ; Search time 55.1894 Seconds
(without alignments)
411.624 Million cell updates/sec

Title: US-09-600-932-2_COPY_47_118

Perfect score: 394

Sequence: 1 GPKGDDGKGPGEKGHK.....DKGKGLGIPGKKGATV 72

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPRENBL_25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	394	100.0	277	4	Q9Y6Z7
2	351	89.1	277	11	Q8CF98
3	351	89.1	277	11	Q8C1C5
4	207	52.5	268	2	Q9F685
5	205	52.0	645	2	Q9KXB9
6	205	52.0	645	9	Q9XJK8
7	205	52.0	645	9	Q7V3C2
8	205	52.0	645	9	Q7Y2W1
9	205	52.0	645	16	Q8XAX7
10	205	52.0	678	9	Q8SCA4
11	196	49.7	1723	5	Q9GQB1
12	195.5	49.6	465	2	Q9AGC4
13	195	49.5	465	12	Q8QTH5
14	194	49.2	271	4	Q9SMP8
15	193.5	49.1	291	2	Q9F690
16	193	49.0	688	11	Q9K2W0

17	193	49.0	688	11	Q07643
18	192	48.7	272	11	Q9DC75
19	191	48.5	271	13	Q7T0T0
20	190.5	48.4	410	2	Q9F691
21	189	48.0	397	2	Q9F686
22	186.5	47.3	1779	5	Q9VMV4
23	185	47.0	396	2	Q9AGC5
24	184.5	46.8	344	9	Q857L6
25	184.5	46.8	1366	4	Q15177
26	184.5	46.8	1366	4	Q7Z5S6
27	184.5	46.8	2551	16	Q8CYI8
28	184	46.7	380	2	Q9F692
29	184	46.7	400	2	Q9F689
30	183.5	46.6	291	5	Q23422
31	183.5	46.6	434	2	Q9ACN4
32	183	46.4	1349	13	Q8AW17
33	182	46.2	1285	16	Q832X8
34	182	46.2	1549	11	Q60444
35	182	46.2	1714	4	Q7Z5L5
36	182	46.2	1827	13	Q8UUM5
37	181.5	46.1	1439	5	O97406
38	181	45.9	690	13	Q8JGL8
39	181	45.9	1684	12	Q8VAA1
40	181	45.9	1684	12	Q8JNB6
41	181	45.9	1684	12	Q91LK9
42	180.5	45.8	660	5	Q86D04
43	180	45.7	181	9	Q9ZXF4
44	180	45.7	444	2	O8RLX7
45	180	45.7	708	13	Q7ZWN8

ALIGNMENTS

RESULT 1

Q9Y6Z7 PRELIMINARY; PRT; 277 AA.

AC Q9Y6Z7; (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Collectin 34.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9240768; PubMed=10224141;
RA Ohtani K., Suzuki Y., Bda S., Kawai T., Kase T., Yamazaki H.,
RA Keshi H., Sakai Y., Fukuoh A., Sakamoto T., Wakamiya N.,
RT "Molecular cloning of a novel collectin from liver (CL-L1).";
RL J. Biol. Chem. 274:13681-13689 (1999).
DR EMBL; AB002631; BAA81747.1; -.
DR HSSP; P19999; 2MSB.
DR Genew; HGNC:2220; COLEC10.
DR GO; GO:0005737; C:cytoplasm; TAS.
DR GO; GO:0005530; F:lectin; TAS.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN_1; 1.
DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
SQ SEQUENCE 277 AA; 30733 MW; 9736861CEBDC5C25 CRC64;

Query Match 100.0%; Score 394; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 5.1e-34;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGDDGKGPGEKGHKYGRMGKIGELGDMGRGNIGTGPIGKKGDKSGKLL 60


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Db 47 GPKGDDDEKDPGEKGKGVGMOPKGIKGBLMDGDRGNIGKTGPIGKKGDKGKGLL 106
QY 61 GIPGEKGKAGTV 72
    |||||
Db 107 GIPGEKGKAGTV 118

RESULT 2
ID Q8CF98 PRELIMINARY; PRT; 277 AA.
AC Q8CF98;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Collectin-L1. (Mouse).
OS Mus musculus
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=22333927; PubMed=12450124;
RA Kawai T., Suzuki Y., Eda S., Kase T., Ohtani K., Sakai Y., Keshi H.,
RA Fukuchi A., Sakamoto T., Nozaki M., Copeland N.G., Jenkins N.A.,
RA Wakamiya N.;
RT "Molecular Cloning of Mouse Collectin Liver 1.";
RL Biosci. Biotechnol. Biochem. 66:2134-2145(2002).
DR EMBL; AB018429; BAC53954.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF00059; lectin c; 1.
DR SMART; SM00034; CLECT_1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS0041; C_TYPE_LLECTIN_2; 1.
DR NCBI_TaxID=10090;
RP SEQUENCE 277 AA; 30524 MW; 58C743A2E07A2872 CRC64;

Query Match 89.1%; Score 351; DB 11; Length 277;
Best Local Similarity 87.5%; Pred. No. 1.9e-29;
Matches 63; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPKGDDDEKDPGEKGKGVGMOPKGIKGBLMDGDRGNIGKTGPIGKKGDKGKGLL 60
Db 47 GPKGDDDEKDPGEKGKGVGMOPKGIKGBLMDGDRGNIGKTGPIGKKGDKGKGLL 106

QY 61 GIPGEKGKAGTV 72
    |||||
Db 107 GIPGEKGKAGTV 118

RESULT 3
ID Q8C1C5 PRELIMINARY; PRT; 277 AA.
AC Q8C1C5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Collectin 34 homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
```

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DR EMBL; AK028423; BAC25941.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF00059; lectin c; 1.
DR SMART; SM00034; CLECT_1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS0041; C_TYPE_LLECTIN_2; 1.
DR NCBI_TaxID=10090;
RP SEQUENCE 277 AA; 30510 MW; 94EF23A2E5404872 CRC64;

Query Match 89.1%; Score 351; DB 11; Length 277;
Best Local Similarity 87.5%; Pred. No. 1.9e-29;
Matches 63; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPKGDDDEKDPGEKGKGVGMOPKGIKGBLMDGDRGNIGKTGPIGKKGDKGKGLL 60
Db 47 GPKGDDDEKDPGEKGKGVGMOPKGIKGBLMDGDRGNIGKTGPIGKKGDKGKGLL 106

QY 61 GIPGEKGKAGTV 72
    |||||
Db 107 GIPGEKGKAGTV 118

RESULT 4
ID Q9F685 PRELIMINARY; PRT; 268 AA.
AC Q9F685;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Collagen-like surface protein (Fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AP55;
RX MEDLINE=20490571; PubMed=11035747;
RA Rasmussen M., Eden A., Bjorck L.;
RT "ScIA, a novel collagen-like surface protein of streptococcus
RT pyogenes.";
RL Infect. Immun. 68:6370-6377(2000).
DR EMBL; AF298338; AAC30218.1; -.
DR InterPro; IPR008160; Collagen.
DR Pfam; PF01391; Collagen; 1.
DR FT NON TER 1
DR FT NON TER 268
DR NCBI_TaxID=1314;
RP SEQUENCE 268 AA; 28668 MW; 2E42FBA768BC6663 CRC64;

Query Match 52.5%; Score 207; DB 2; Length 268;
Best Local Similarity 64.1%; Pred. No. 3.6e-14;
Matches 41; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

QY 7 GEKGDPEGEKGKGVGMOPKGIKGBLMDGDRGNIGKTGPIGKKGDKGKGLLGPGEK 66
Db 109 GEKGDPEGEKGKGVGMOPKGIKGBLMDGDRGNIGKTGPIGKKGDKGKGLLGPGEK 168

QY 67 GKAG 70
    |||
Db 169 GPAG 172

RESULT 5
ID Q9KXB9 PRELIMINARY; PRT; 645 AA.
AC Q9KXB9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tail fiber protein.
OS H0137.
```

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OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7; PubMed=10734605;
RX MEDLINE=20198780; Kubota Y., Yutsudo C.H., Kimura S.,
RA Makino K., Yokoyama K., Kubota Y., Hattori M., Tatsuno I., Abe H., Iida T.,
RA Kurokawa K., Ishii K., Hayashi T., Yasunaga T., Honda T.,
RA Yamamoto K., Ohnishi M., Hayashi T., Yasunaga T., Honda T.,
RA Sasaki K., Shinagawa H.;
RT "Complete nucleotide sequence of the prophage VT2-Sakai carrying the
RT verotoxin 2 genes of the enterohemorrhagic Escherichia coli O157:H7
RT derived from the Sakai outbreak.";
RL Genes Genet. Syst. 74:227-239(1999).
DR EMBL; AF000422; BA94165.1; -.
DR InterPro; IPR008969; Carboxypeptid_reg.
DR InterPro; IPR008161; C1g_helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR005068; Phage_fiber_2.
DR Pfam; PF01391; Collagen; 4.
DR Pfam; PF03406; Phage_fiber_2; 1.
DR ProDom; PD000007; C1g_helix; 2.
SQ SEQUENCE 645 AA; 63954 MW; 7B31B1957E1F499C CRC64;

Query Match 52.0%; Score 205; DB 2; Length 645;
Best Local Similarity 54.3%; Pred. No. 1.6e-13;
Matches 38; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 1 GPKGDDGEGKDPGEGKHGKVGKMGPKGKIGELGMDGRNIGKTGPIGKKGKGGKGLL 60
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
247 GPQGETGPKGDVGPKGTEGVPVGPQGPAGPKGERGVDVGAQGVAGPAGPRGKGQGERGPQ 306

QY 61 GIPGKKGKAG 70
Db |||||

RESULT 6
ID Q9XJK8 PRELIMINARY; PRT; 645 AA.
AC Q9XJK8;
DT 01-NOV-1999 (T-EMBLrel. 12, Created)
DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Putative tail fiber protein.
GN L0121.
OS Bacteriophage 933W, and
OS Bacteriophage VT2-Sa.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC Lambda-like viruses.
OX NCBI_TaxID=10730, 97081;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Phage 933W;
RX MEDLINE=99173898; PubMed=10074068;
RA Plunkett G III; Rose D.J., Duffee T.J., Blattner F.R.;
RT "Sequence of Shiga toxin 2 phage 933W from Escherichia coli O157:H7;
RT Shiga toxin as a phage late-gene product.";
RL J. Bacteriol. 181:1767-1778(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Phage 933W;
RA Plunkett G III;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBSJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Phage VT2-Sa;
RA Miyamoto H.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBSJ databases.
RN [4]
RP SEQUENCE FROM N.A.
```

```
RC SPECIES=Phage VT2-Sa;
RX MEDLINE=99419919; PubMed=10492170;
RA Miyamoto H., Nakai W., Yajima N., Fujibayashi A., Higuchi T., Sato K.,
RA Matsushiro A.;
RT "Sequence analysis of Stx2-Converting phage VT2-Sa shows a great
RT divergence in early regulation and replication regions.";
RL DNA Res. 6:235-240(1999).
DR EMBL; AF125520; AAD25464.1; -.
DR EMBL; AF000363; BAA84341.1; -.
DR InterPro; IPR008969; Carboxypeptid_reg.
DR InterPro; IPR008161; C1g_helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR005068; Phage_fiber_2.
DR Pfam; PF01391; Collagen; 4.
DR Pfam; PF03406; Phage_fiber_2; 1.
DR ProDom; PD000007; C1g_helix; 2.
KW Hypothetical protein.
SQ SEQUENCE 645 AA; 63955 MW; DB360743A572FF4A CRC64;

Query Match 52.0%; Score 205; DB 9; Length 645;
Best Local Similarity 54.3%; Pred. No. 1.6e-13;
Matches 38; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 1 GPKGDDGEGKDPGEGKHGKVGKMGPKGKIGELGMDGRNIGKTGPIGKKGKGGKGLL 60
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
247 GPQGETGPKGDVGPKGTEGVPVGPQGPAGPKGERGVDVGAQGVAGPAGPRGKGQGERGPQ 306

QY 61 GIPGKKGKAG 70
Db |||||

RESULT 7
ID Q7Y3C2 PRELIMINARY; PRT; 645 AA.
AC Q7Y3C2;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Stx1 converting bacteriophage.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC Lambda-like viruses.
OX NCBI_TaxID=194948;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Stx1 phage;
RX MEDLINE=22697399; PubMed=12813092;
RA Sato T., Shimizu T., Watarai M., Kobayashi M., Kano S., Hamabata T.,
RA Takeda Y., Yamasaki S.;
RT "Genome Analysis of a Novel Shiga Toxin 1 (Stx1)-Converting Phage
RT Which Is Closely Related to Stx2-Converting Phages but Not to Other
RT Stx1-Converting Phages.";
RL J. Bacteriol. 185:3966-3971(2003).
DR EMBL; AF005153; BAC7836.1; -.
KW Hypothetical protein.
SQ SEQUENCE 645 AA; 63955 MW; DB360743A572FF4A CRC64;

Query Match 52.0%; Score 205; DB 9; Length 645;
Best Local Similarity 54.3%; Pred. No. 1.6e-13;
Matches 38; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 1 GPKGDDGEGKDPGEGKHGKVGKMGPKGKIGELGMDGRNIGKTGPIGKKGKGGKGLL 60
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
247 GPQGETGPKGDVGPKGTEGVPVGPQGPAGPKGERGVDVGAQGVAGPAGPRGKGQGERGPQ 306

QY 61 GIPGKKGKAG 70
Db |||||

RESULT 8
Q7Y2W1
```


Q9GQB1 PRELIMINARY; PRT; 1723 AA.

AC Q9GQB1
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Type IV collagen alpha 1 chain precursor.
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Chordata; Hydrozoa; Hydrozoa; Anthomedusae;
OC Hydridae; Hydra.
OX NCBI_TaxID=6087;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20564332; PubMed=10956657;
RA Fowler S.J., Jose S., Zhang X., Deutzmann R., Sarraz M.P. Jr.,
RA Boot-Handford R.P.;
RT "Characterization of hydra type IV collagen: Type IV collagen is
RT essential for head regeneration and its expression is up-regulated
RT upon exposure to glucose."
RL J. Biol. Chem. 275:39589-39599(2000).
DR EMBL: AF282902; AAG40729.1; -
DR GO: 0005581; C:collagen; IEA.
DR GO: 0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro: IPR008161; Clg_helix.
DR InterPro: IPR008160; Collagen.
DR InterPro: IPR001442; Procollagen4_C.
DR Pfam: PF01413; C4; 2.
DR ProDom: PD000007; Clg_helix; 6.
DR ProDom: PD003923; Procollagen4; 1.
DR SMART: SM00111; C4; 2.
DR Collagen; Signal.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 1723 AA; 168996 MW; 92496D62FD162F01 CRC64;
POTENTIAL.
1 24
Query Match 49.7%; Score 196; DB 5; Length 1723;
Best Local Similarity 38.9%; Pred. No. 4.2e-12;
Matches 42; Conservative 13; Mismatches 15; Indels 38; Gaps 3;
1 GPKGDGEGKDP---GEEGKHGKVRMGPKIGKE-----LQDMGDRGNIGKTG 46
173 GPKSQDGPAGDPGTGDKGESSKAGRMGPGQLRGKRGAGDSNITIFGERGKDIGLPG 232
47 P-----IGKKDKGKGLLIGIPGEGKAG 70
233 PFERDNGSSVTGELITNIQPKGQKGGQKGGQKGGQKGGQKGGQKGGQKGGQKGGQ 280

Q9AGC4 PRELIMINARY; PRT; 465 AA.

AC Q9AGC4
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Collagen-like protein B (Fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=AP55;
RA Rasmussen M., Bjorck L.;
RT "Phase-variation of a novel collagen-like surface protein in
RT Streptococcus pyogenes."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF336819; AAK30079.1; -
DR InterPro: IPR008161; Clg_helix.
DR InterPro: IPR008160; Collagen.
DR Pfam: PF01391; Collagen; 5.
DR ProDom: PD000007; Clg_helix; 1.
NON_TER 465 465

Q9 SEQUENCE 465 AA; 46694 MW; 0A3A499F897BE7AF CRC64;

Query Match 49.6%; Score 195.5; DB 2; Length 465;
Best Local Similarity 47.3%; Pred. No. 1.1e-12;
Matches 43; Conservative 5; Mismatches 22; Indels 21; Gaps 2;
1 GPKGDGEGKDPGEGKHGKVRMGPK-----GKGLGDMGDRGNIGKTGPI 48
113 GKSGDPGEGKDPGEGKATGQVGPGRGKDPGEGKATGQVGPGRGKDPGEGKATG 172
49 GKKGDKGKGLL-----GIPGEGKAG 70
173 GKSGDPGEGKATGQVGPGRGKDPGEGKATG 203

RESULT 13

Q8QTH5 PRELIMINARY; PRT; 465 AA.

AC Q8QTH5
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE WSSV021.
OS White spot syndrome virus (WSSV).
OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae.
OX NCBI_TaxID=92652;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Taiwan;
RX MEDLINE=20517548; PubMed=11062040;
RA Tsai M.F., Yu H.T., Tzeng H.F., Leu J.H., Chou C.M., Huang C.J.,
RA Wang C.H., Lin J.Y., Kou G.H., Lo C.F.;
RT "Identification and characterization of a shrimp white spot syndrome
RT virus (WSSV) gene that encodes a novel chimeric polypeptide of
RT cellular-type thymidine kinase and thymidylate kinase."
RL Virology 277:100-110(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Taiwan;
RX MEDLINE=21844071; PubMed=11853398;
RA Chen L.L., Leu J.H., Huang C.J., Chou C.M., Chen S.M., Wang C.H.,
RA Lo C.F., Kou G.H.;
RT "Identification of a nucleocapsid protein (VP35) gene of shrimp white
RT spot syndrome virus and characterization of the motif important for
RT targeting VP35 to the nuclei of transfected insect cells."
RL Virology 293:44-53(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Taiwan;
RA Lo C.-F., Kou G.-H.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF440570; AAL88889.1; -
DR InterPro: IPR008160; Collagen.
DR Pfam: PF01391; Collagen; 2.
SQ SEQUENCE 465 AA; 53009 MW; 435F1A3488B83BD5 CRC64;

Query Match 49.5%; Score 195; DB 12; Length 465;
Best Local Similarity 52.9%; Pred. No. 1.3e-12;
Matches 37; Conservative 12; Mismatches 21; Indels 0; Gaps 0;
1 GPKGDGEGKDPGEGKHGKVRMGPKIGKGLGDMGDRGNIGKTGPIGKKGKGLL 60
19 GKSGDKGKGLL-----GIPGEGKAG 70
61 GIPGEGKAG 70
79 GKSGDKGKGLL-----GIPGEGKAG 88

RESULT 14

Q9BWP8 PRELIMINARY; PRT; 271 AA.

ID Q9BWP8
AC Q9BWP8

QY 58 GLIGIPGEKKGAG 70
DB 190 GAQGPAGPQGEAG 202
Search completed: March 8, 2004, 12:15:12
Job time : 57.1894 secs

01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC000078; AAH00078.1; -.
DR HSSP; P22897; IEGG.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF00059; lectin c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 271 AA; 28665 MW; A14A248CE41DB340 CRC64;
Query Match 49.2%; Score 194; DB 4; Length 271;
Best Local Similarity 52.1%; Pred. No. 8.8e-13;
Matches 38; Conservative 12; Mismatches 17; Indels 6; Gaps 2;
QY 1 GPKGDDGEGKDGEGKGVGMGPKIGKELGDMGDRGNI---GKTGPIGKKGKGEK 57
DB 41 GLKGDAGEKGD---KGAPGRGVGTGKGDGMDGKQKQSVGRHKGPIGSGKGEKGS 97
QY 58 GLIGIPGEKKGAG 70
DB 98 GDIGPEPFGNGEPG 110
RESULT 15
ID Q3F690 PRELIMINARY; PRT; 291 AA.
AC Q3F690;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Collagen-like surface protein (Fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AP15;
RX MEDLINE=20490571; PubMed=11035747;
RA Rasmussen M.; Eden A.; Bjorck L.;
RT "ScLA, a novel collagen-like surface protein of streptococcus
pyogenes.";
RL Infect. Immun. 68:6370-6377(2000).
DR EMBL; AF296333; AAG30213.1; -.
DR InterPro; IPR008160; Collagen.
DR Pfam; PF01391; Collagen; 1.
DR NON_TER 1
FT NON_TER 291 291
SQ SEQUENCE 291 AA; 31100 MW; E879218AEA003349 CRC64;
Query Match 49.1%; Score 193.5; DB 2; Length 291;
Best Local Similarity 53.4%; Pred. No. 1.1e-12;
Matches 39; Conservative 7; Mismatches 24; Indels 3; Gaps 1;
QY 1 GPKGDDGEGKGD---PGEHGHGVGMGPKIGKELGDMGDRGNI---GKTGPIGKKGKGEK 57
DB 130 GPKGDRGEGKDTGATGPGQAGKDGAPGKDGKGDGEGTGAQGPVGPQGEKGET 189


```
CC CC      intervertebral disc disease (IDD) [MIM:603932]. IDD is one of the
CC CC      most common musculo-skeletal disorders.
CC CC      -1- SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH
CC CC      INTERRUPTED HELICES (FACIT) FAMILY.
CC CC      -----
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CC CC      -----
CC CC      EMBL; AF019406; AAC33512.1; -.
CC CC      EMBL; AL050341; CB881511.1; -.
CC CC      EMBL; M95610; AAA80977.1; -.
CC CC      Genew; HGNC:2218; COL9A2.
CC CC      MIM; 120260; -.
CC CC      MIM; 600204; -.
CC CC      MIM; 603932; -.
CC CC      GO; GO:0005594; C:collagen type IX; TAS.
CC CC      GO; GO:001501; P:skeletal development; TAS.
CC CC      InterPro; IPR008161; C1g_helix.
CC CC      Pfam; PF01391; Collagen; 9.
CC CC      ProDom; PD000007; C1g_helix; 1.
CC CC      Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
CC CC      Collagen; Signal; Glycoprotein; Proteoglycan; Disease mutation;
CC CC      Polymorphism.
CC CC      SIGNAL      1 23      POTENTIAL.
CC CC      CHAIN      24 689      COLLAGEN ALPHA 2 (IX) CHAIN.
CC CC      DOMAIN      27 163      TRIPLE-HELICAL REGION 1.
CC CC      DOMAIN      164 180      NON-HELICAL REGION 1.
CC CC      DOMAIN      181 519      TRIPLE-HELICAL REGION 2.
CC CC      DOMAIN      520 549      NON-HELICAL REGION 2.
CC CC      DOMAIN      550 632      TRIPLE-HELICAL REGION 3.
CC CC      DOMAIN      633 634      NONHELICAL REGION 3.
CC CC      DOMAIN      635 664      TRIPLE-HELICAL REGION 4.
CC CC      DOMAIN      665 689      NONHELICAL REGION 4.
CC CC      DISULFID      174 174      INTERCHAIN (POTENTIAL).
CC CC      DISULFID      178 178      INTERCHAIN (POTENTIAL).
CC CC      CARBOHYD      169 169      O-LINKED (GLYCOSAMINOGLYCAN) (BY
CC CC      VARIANT      326 326      Q -> R.
CC CC      VARIANT      326 326      /FTid=VAR 012659.
CC CC      Q -> W (in IDD; requires 2 nucleotide
CC CC      substitutions).
CC CC      /FTid=VAR 012658.
CC CC      SEQUENCE      689 AA; 65131 MW; EB6106502F6FA862 CRC64;
CC CC      Query Match      49.78; Score 196; DB 1; Length 689;
CC CC      Best Local Similarity      51.44; Pred. No. 2.5e-12;
CC CC      Matches      36; Conservative      13; Mismatches      21; Indels      0; Gaps      0;
CC CC      QY      1      GPKGDDEKGPGEKGKGVGMGPKGKGLGMDGRNIGTKGPGIKKDKGKGLL 60
CC CC      DB      355      GPQGLPGSPGPKGEGPGRGIRGIGQGMGQKDGQGVGPQPGQKPGKGEQGP 414
CC CC      QY      61      GIPGEKQKAG 70
CC CC      DB      415      GIPGPGQLPG 424
CC CC      RESULT 2
CC CC      CA29_MOUSE      STANDARD; PRT; 688 AA.
CC CC      AC      Q07643;
CC CC      DT      15-MAR-2004 (Rel. 43, Created)
CC CC      DT      15-MAR-2004 (Rel. 43, Last sequence update)
CC CC      DT      15-MAR-2004 (Rel. 43, Last annotation update)
CC CC      DE      Collagen alpha 2 (IX) chain precursor.
CC CC      GN      COL9A2
CC CC      OS      Mus musculus (Mouse).
```

```
OC CC      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC CC      Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
OC CC      NCBI_TaxID=10090;
OC CC      [1]
OC CC      RP      SEQUENCE FROM N.A.
OC CC      RC      STRAIN=BALE/c; TISSUE=Liver;
OC CC      RX      MEDLINE=94148964; PubMed=8106484;
OC CC      RA      Perla M., Elima K., Metsaranta M., Rosati R., de Crombrughe B.,
OC CC      Vuorio E.;
OC CC      RT      "The exon structure of the mouse alpha 2 (IX) collagen gene shows
OC CC      RT      unexpected divergence from the chick gene.";
OC CC      J. Biol. Chem. 269:5064-5071(1994).
OC CC      [2]
OC CC      RN      SEQUENCE OF 521-568 FROM N.A.
OC CC      RC      STRAIN=C57BL/6;
OC CC      RX      MEDLINE=92182017; PubMed=1543751;
OC CC      RA      Elima K., Metsaranta M., Kallio J., Peraelae M., Eroola I.,
OC CC      Garofalo S., de Crombrughe B., Vuorio E.;
OC CC      RT      "Specific hybridization probes for mouse alpha 2 (IX) and alpha 1 (X)
OC CC      RT      collagen mRNAs.";
OC CC      Biochim. Biophys. Acta 1130:78-80(1992).
OC CC      -1- FUNCTION: Structural component of hyaline cartilage and vitreous
OC CC      of the eye.
OC CC      -1- SUBUNIT: Heterotrimer of an alpha 1 (IX), an alpha 2 (IX) and an
OC CC      alpha 3 (IX) chain.
OC CC      -1- PTM: Covalently linked to the telopeptides of type II collagen by
OC CC      lysine-derived cross-links.
OC CC      -1- PTM: Prolines at the third position of the tripeptide repeating
OC CC      unit (G-X-Y) are hydroxylated in some or all of the chains.
OC CC      -1- SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH
OC CC      INTERRUPTED HELICES (FACIT) FAMILY.
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OC CC      or send an email to license@isb-sib.ch).
OC CC      -----
OC CC      EMBL; Z22923; CAA80503.1; -.
OC CC      EMBL; X63014; CAA44742.1; -.
OC CC      PIR; A53330; A53330.
OC CC      MGD; MGI:88466; Col9a2.
OC CC      InterPro; IPR000637; AT hook.
OC CC      InterPro; IPR008161; C1g_helix.
OC CC      InterPro; IPR008160; Collagen.
OC CC      Pfam; PF01391; Collagen; 9.
OC CC      PRINTS; PR00929; ATHOOK.
OC CC      ProDom; PD000007; C1g_helix; 3.
OC CC      Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
OC CC      Collagen; Signal; Glycoprotein; Proteoglycan.
OC CC      SIGNAL      1 22      POTENTIAL.
OC CC      CHAIN      23 688      COLLAGEN ALPHA 2 (IX) CHAIN.
OC CC      DOMAIN      26 162      TRIPLE-HELICAL REGION 1.
OC CC      DOMAIN      163 179      NON-HELICAL REGION 1.
OC CC      DOMAIN      180 518      TRIPLE-HELICAL REGION 2.
OC CC      DOMAIN      519 548      NON-HELICAL REGION 2.
OC CC      DOMAIN      549 631      TRIPLE-HELICAL REGION 3.
OC CC      DOMAIN      632 633      NONHELICAL REGION 3.
OC CC      DOMAIN      634 663      TRIPLE-HELICAL REGION 4.
OC CC      DOMAIN      664 688      NONHELICAL REGION 4.
OC CC      DISULFID      173 173      INTERCHAIN (POTENTIAL).
OC CC      DISULFID      177 177      INTERCHAIN (POTENTIAL).
OC CC      CARBOHYD      168 168      O-LINKED (GLYCOSAMINOGLYCAN) (BY
OC CC      SIMILARITY).
OC CC      VARIANT      525 525      V -> M (IN STRAIN C57BL).
OC CC      VARIANT      610 610      H -> R (IN STRAIN C57BL).
OC CC      VARIANT      666 666      A -> G (IN STRAIN C57BL).
OC CC      SEQUENCE      688 AA; 65322 MW; 7C7A73D2CD2A039F CRC64;
OC CC      Query Match      49.0%; Score 193; DB 1; Length 688;
OC CC      Best Local Similarity      45.1%; Pred. No. 5.2e-12;
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Matches 37; Conservative 14; Mismatches 19; Indels 12; Gaps 1;
QY 1 GKQGDGKGDGGE-----BKHKGVKRMKPKIGKGLGMDGRGNIGTGP 48
DB 342 GYKGGFGDKGEGQGLPGVSPGKGEPRGEGIGQGGQGGGPGVGPQ 401
QY 49 GKQGDGKGLGIPGKKGAG 70
DB 402 GYKGGFGDKGEGQGLPGVSPGKGEPRGEGIGQGGQGGGPGVGPQ 423
RESULT 3
CA14 DROME STANDARD; PRT; 1775 AA.
AC P08120;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Collagen alpha 1(IV) chain precursor.
GN CG25C OR DCG1.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89054012; PubMed=3142875;
RA Blumberg B., Mackrell A.J., Fessler J.H.;
RT "Drosophila basement membrane procollagen alpha 1(IV). II. Complete
RT cDNA sequence, genomic structure, and general implications for
RT supramolecular assemblies.";
RL J. Biol. Chem. 263:18328-18337 (1988).
RN [2]
RP SEQUENCE FROM N.A.
RX Blumberg B.;
RA Thesis (1987), University of California / Los Angeles, U.S.A.
RN [3]
RP SEQUENCE FROM N.A.
RA Mackrell A.J.;
RN [4]
RP SEQUENCE OF 1065-1775 FROM N.A.
RX MEDLINE=87194801; PubMed=3106346;
RA Blumberg B., Mackrell A.J., Olson P.F., Kurkinen M., Monson J.M.,
RA Natzie J.E., Fessler J.H.;
RT "Basement membrane procollagen IV and its specialized carboxyl domain
RT are conserved in Drosophila, mouse, and human.";
RL J. Biol. Chem. 262:5947-5950 (1987).
RN [5]
RP SEQUENCE OF 1355-1775 FROM N.A.
RX MEDLINE=87246644; PubMed=3109906;
RA Cecchini J.P., Knibiehler B., Mirre C., le Parco Y.;
RT "Evidence for a type-IV-related collagen in Drosophila melanogaster.
RT Evolutionary constancy of the carboxyl-terminal noncollagenous
RT domain.";
RL Eur. J. Biochem. 165:587-593 (1987).
RN [6]
RP SEQUENCE OF 762-1230 FROM N.A.
RX MEDLINE=82197577; PubMed=6210912;
RA Monson J.M., Natzie J., Friedman J., McCarthy B.J.;
RT "Expression and novel structure of a collagen gene in Drosophila.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:1761-1765 (1982).
CC -1- FUNCTION: Collagen type IV is specific for basement membranes.
CC -1- SUBUNIT: Trimers of two alpha 1(IV) and one alpha 2(IV) chain.
CC Type IV collagen forms a mesh-like network linked through
CC intermolecular interactions between 7S domains and between NCI
CC domains.
CC -1- DOMAIN: Alpha chains of type IV collagen have a noncollagenous
CC domain (NC1) at their C-terminus, frequent interruptions of the G-
CC X-Y repeats in the long central triple-helical domain (which may
CC cause flexibility in the triple helix), and a short N-terminal
CC triple-helical 7S domain.

CC -1- PTM: Prolines at the third position of the tripeptide repeating
CC unit (G-X-Y) are hydroxylated in some or all of the chains.
CC -1- PTM: Type IV collagens contain numerous cysteine residues which
CC are involved in inter- and intramolecular disulfide bonding. 12 of
CC these, located in the NC1 domain, are conserved in all known type
CC IV collagens.
CC
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CC
CC EMBL; M23704; AAA28404.1; -;
CC EMBL; M96575; AAB59184.1; -;
CC EMBL; J02727; AAA28423.1; -;
CC EMBL; M28334; AAA28422.1; -;
CC EMBL; V00200; CAA23486.2; -;
CC PIR; A31893; A31893.
CC FlyBase; FBgn0000289; Cg25C.
CC GO; GO:0005597; C:collagen type IV; NAS.
CC InterPro; IPR008161; Clg_helix.
CC InterPro; IPR008160; Collagen.
CC InterPro; IPR001442; Procollagn4_C.
CC Pfam; PF01413; C4; 2.
CC Pfam; PF01391; Collagen; 25.
CC ProDom; PD000007; Clg_helix; 9.
CC ProDom; PD003923; Procollagn4; 1.
CC SMART; SM00111; C4; 2.
CC Extracellular matrix; Connective tissue; Basement membrane;
KW Repeat; Hydroxylation; Glycoprotein; Collagen; Signal.
FT SIGNAL 1 23
FT PROPEP 24 ?
FT CHAIN ? 1775 AMINO-TERMINAL PROPEPTIDE (7S DOMAIN).
FT DOMAIN ? 1544 COLLAGEN ALPHA 1(IV) CHAIN.
FT DOMAIN 1545 1775 TRIPLE-HELICAL REGION.
FT DISULFID 1549 1655 NONHELICAL REGION (NC1).
FT DISULFID 1569 1655 OR 1652 (BY SIMILARITY).
FT DISULFID 1599 1652 OR 1655 (BY SIMILARITY).
FT DISULFID 1611 1617 BY SIMILARITY.
FT DISULFID 1674 1770 OR 1767 (BY SIMILARITY).
FT DISULFID 1708 1767 OR 1770 (BY SIMILARITY).
FT DISULFID 1720 1727 BY SIMILARITY.
FT CARBOHYD 72 72 N-LINKED (GLCNAC...) (PROBABLE).
FT CONFLICT 948 948 L -> S (IN REF. 6).
FT CONFLICT 997 997 S -> T (IN REF. 6).
FT CONFLICT 1357 1357 Q -> K (IN REF. 5).
FT CONFLICT 1360 1360 Q -> K (IN REF. 5).
FT CONFLICT 1373 1373 T -> I (IN REF. 5).
FT CONFLICT 1496 1496 L -> R (IN REF. 5).
FT CONFLICT 1507 1511 ETGNV -> RAGOR (IN REF. 5).
FT CONFLICT 1529 1529 E -> K (IN REF. 5).
FT CONFLICT 1733 1733 M -> I (IN REF. 5).
SQ SEQUENCE 1775 AA; 174119 MW; 2D5EAB23149525CD CRC64;
Query Match 47.3%; Score 186.5; DB 1; Length 1775;
Best Local Similarity 46.8%; Pred. No. 5.7e-11;
Matches 37; Conservative 10; Mismatches 23; Indels 9; Gaps 1;
QY 1 GKQGDGGE-----KGDGEGKGVKRMKPKIGKGLGMDGRGNIGTGP 51
DB 295 GYKGGFGDKGEGQGLPGVSPGKGEPRGEGIGQGGQGGGPGVGPQ 354
QY 52 GYKGGFGDKGEGQGLPGVSPGKGEPRGEGIGQGGQGGGPGVGPQ 354
DB 355 GYKGGFGDKGEGQGLPGVSPGKGEPRGEGIGQGGQGGGPGVGPQ 373
RESULT 4
CA21 HUMAN STANDARD; PRT; 1366 AA.
ID CA21 HUMAN
AC P08123; P02464; Q9UEB6; Q9UPH0;

DT 01-AUG-1988 (Rel. 08, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Collagen alpha 2(I) chain precursor.
GN COL1A2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=8058962; PubMed=2824475;
RA de Wet W.J., Bernard M.P., Benson-Chanda V., Chu M.-L., Dickson L.A.,
RA Weil D., Ramirez F.;
RT "Organization of the human pro-alpha 2(I) collagen gene.";
RL J. Biol. Chem. 262:16032-16036(1987).
RN [2]
RN SEQUENCE FROM N.A.
RA Korkko J.M., Earley J.J., Ala-Kokko L., Prockop D.J.;
RT "Analysis of the COL1A1 and COL1A2 genes by CSGE and DNA sequencing in
RT 14 patients with mild OI (Type I). Identification of common sequences
RT for null allele mutations.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE OF 1-765 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=88339824; PubMed=3421913;
RA Kuivaniemi H., Tromp G., Chu M.-L., Prockop D.J.;
RT "Structure of a full-length cDNA clone for the propro alpha 2(I)
RT chain of human type I procollagen. Comparison with the chicken gene
RT confirms unusual patterns of gene conservation.";
RL Biochem. J. 252:633-640(1988).
RN [4]
RN SEQUENCE OF 181-1366 FROM N.A.
RA Kalicki J., Wamsley P., Gibson A.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RN SEQUENCE OF 623-1366 FROM N.A.
RX MEDLINE=83178919; PubMed=6687691;
RA Bernard M.P., Myers J.C., Chu M.-L., Ramirez F., Eikenberry E.F.,
RA Prockop D.J.;
RT "Structure of a cDNA for the pro alpha 2 chain of human type I
RT procollagen. Comparison with chick cDNA for pro alpha 2(I) identifies
RT structurally conserved features of the protein and the gene.";
RL Biochemistry 22:1139-1145(1983).
RN [6]
RN SEQUENCE OF 80-96.
RC TISSUE=Skin;
RX MEDLINE=71038625; PubMed=5529814;
RA Click E.M., Bornstein P.;
RT "Isolation and characterization of the cyanogen bromide peptides from
RT the alpha 1 and alpha 2 chains of human skin collagen.";
RL Biochemistry 9:4693-4706(1970).
RN [7]
RN SEQUENCE OF 417-447.
RC TISSUE=Skin;
RX MEDLINE=75008198; PubMed=4412529;
RA Fietzek P.P., Furthmayr H., Kuehn K.;
RT "Comparative sequence studies on alpha2-CB2 from calf, human, rabbit
RT and p-g-skin collagen.";
RL Eur. J. Biochem. 47:257-261(1974).
RN [8]
RN SEQUENCE OF 145-198 FROM N.A.
RX MEDLINE=88298792; PubMed=3403536;
RA Kuivaniemi H., Sabol C., Tromp G.;
RT "A 19-base pair deletion in the pro-alpha 2(I) gene of type I
RT procollagen that causes in-frame RNA splicing from exon 10 to exon 12
RT in a proband with atypical osteogenesis imperfecta and in his
RT asymptomatic mother.";
RL J. Biol. Chem. 263:11407-11413(1988).
RN [9]
RN SEQUENCE OF 960-1351 FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=90304220; PubMed=2364107;
RA Maekelae J.K., Vuorio T., Vuorio E.;
RT "Growth-dependent modulation of type I collagen production and mRNA
RT levels in cultured human skin fibroblasts.";
RL Biochim. Biophys. Acta 1049:171-176(1990).
RN [10]
RN REVIEW ON VARIANTS.
RX MEDLINE=91184577; PubMed=2010058;
RA Kuivaniemi H., Tromp G., Prockop D.J.;
RT "Mutations in collagen genes: causes of rare and some common diseases
RT in humans.";
RL FASEB J. 5:2052-2060(1991).
RN [11]
RN REVIEW ON VARIANTS.
RX MEDLINE=97255959; PubMed=3101290;
RA Kuivaniemi H., Tromp G., Prockop D.J.;
RT "Mutations in fibrillar collagens (types I, II, III, and XI), fibril-
RT associated collagen (type IX), and network-forming collagen (type X)
RT cause a spectrum of diseases of bone, cartilage, and blood vessels.";
RL Hum. Mutat. 9:300-315(1997).
RN [12]
RN REVIEW ON OI VARIANTS.
RX MEDLINE=91374476; PubMed=1895312;
RA Byers P.H., Wallis G.A., Willing M.C.;
RT "Osteogenesis imperfecta: translation of mutation to phenotype.";
RL J. Med. Genet. 28:433-442(1991).
RN [13]
RN REVIEW ON OI VARIANTS.
RX MEDLINE=97169389; PubMed=9016532;
RA Dalgleish R.;
RT "The human type I collagen mutation database.";
RL Nucleic Acids Res. 25:181-187(1997).
RN [14]
RN VARIANT EDS-VII-A2.
RX MEDLINE=88059013; PubMed=3680255;
RA Wirtz M.K., Glanville R.W., Steinmann B., Rao V.H., Hollister D.W.;
RT "Ehlers-Danlos syndrome type VIIB. Deletion of 18 amino acids
RT comprising the N-telopeptide region of a pro-alpha 2(I) chain.";
RL J. Biol. Chem. 262:16376-16385(1987).
RN [15]
RN SEQUENCE OF 1090-1107 FROM N.A., AND VARIANT OI-IV ARG-1102.
RX MEDLINE=88227975; PubMed=2897363;
RA Wenstrup R.J., Cohn D.H., Cohen T., Byers P.H.;
RT "Arginine for glycine substitution in the triple-helical domain of
RT the products of one alpha 2(I) collagen allele (COL1A2) produces the
RT osteogenesis imperfecta type IV phenotype.";
RL J. Biol. Chem. 263:7734-7740(1988).
RN [16]
RN VARIANT OI-II ASP-997.
RX MEDLINE=89123407; PubMed=2914942;
RA Baldwin C.T., Constantinou C., Dumars K.W., Prockop D.J.;
RT "A single base mutation that converts glycine 907 of the alpha 2(I)
RT chain of type I procollagen to aspartate in a lethal variant of
RT osteogenesis imperfecta. The single amino acid substitution near the
RT carboxyl terminus destabilizes the whole triple helix.";
RL J. Biol. Chem. 264:3002-3006(1989).
RN [17]
RN VARIANT OI-II SER-955.
RX MEDLINE=89380165; PubMed=2777764;
RA Lamande S.R., Dahl H.-H.M., Cole W.G., Bateman J.F.;
RT "Characterization of point mutations in the collagen COL1A1 and
RT COL1A2 genes causing lethal perinatal osteogenesis imperfecta.";
RL J. Biol. Chem. 264:15809-15812(1989).
RN [18]
RN VARIANT OI-II CYS-877.
RA Fertala A., Westerhausen A., Morris G.M., Rooney J.E., Prockop D.J.;
RT "Two cysteine substitutions in the type I procollagen genes (COL1A1
RT and COL1A2) that cause lethal osteogenesis imperfecta. The location
RT of glycine substitutions does not in any simple way predict their
RT effects on protein function or phenotype.";
RL Am. J. Hum. Genet. 47:A216-A216(1990).
RN [19]
RN VARIANT EDS-VII-A2.
RX

XX MEDLINE=90368825; PubMed=2394758;
RA Weil D., D'Alessio M., Ramirez F., Eyre D.R.;
RT "Structural and functional characterization of a splicing mutation in
RT the pro-alpha 2(I) collagen gene of an Ehlers-Danlos type VII
RT patient.";
RL J. Biol. Chem. 265:16007-16011(1990).
RN [20]
RP VARIANT OI-IV VAL-676.
RX MEDLINE=91291136; PubMed=2064612;
RA Bateman J.F., Hannagan M., Chan D., Cole W.G.;
RT "Characterization of a type I collagen alpha 2(I) glycine-586 to
RT valine substitution in osteogenesis imperfecta type IV. Detection of
RT the mutation and prenatal diagnosis by a chemical cleavage method.";
RL Biochem. J. 276:765-770(1991).
RN [21]
RP VARIANTS OI CYS-349 AND CYS-736.
RX MEDLINE=91115889; PubMed=1990009;
RA Wensrup R.J., Shrago-Howe A.W., Lever L.W., Phillips C.L.,
RA Byers P.H., Cohn D.H.;
RT "The effects of different cysteine for glycine substitutions within
RT alpha 2(I) chains. Evidence of distinct structural domains within the
RT type I collagen triple helix.";
RL J. Biol. Chem. 266:2590-2594(1991).
RN [22]
RP VARIANT OI-II ARG-784.
RX MEDLINE=91340689; PubMed=1874719;
RA Tsuneyoshi T., Westerhausen A., Constantinou C.D., Prockop D.J.;
RT "Substitutions for glycine alpha 1-637 and glycine alpha 2-694 of
RT type I procollagen in lethal osteogenesis imperfecta. The
RT conformational strain on the triple helix introduced by a glycine
RT substitution can be transmitted along the helix.";
RL J. Biol. Chem. 266:15608-15613(1991).
RN [23]
RP VARIANT OI-IV SER-751.
RX MEDLINE=91271401; PubMed=2052622;
RA Spotila L.D., Constantinou C.D., Sereda L., Ganguly A., Riggs B.L.,
RA Prockop D.J.;
RT "Mutation in a gene for type I procollagen (COL1A2) in a woman with
RT postmenopausal osteoporosis: evidence for phenotypic and genotypic
RT overlap with mild osteogenesis imperfecta.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:5423-5427(1991).
RN [24]
RP VARIANT OI-II ARG-547.
RX MEDLINE=93244482; PubMed=1284475;
RA Bateman J.F., Moeller I., Hannagan M., Chan D., Cole W.G.;
RT "Lethal perinatal osteogenesis imperfecta due to a type I collagen
RT alpha 2(I) Gly to Arg substitution detected by chemical cleavage of
RT an mRNA: cDNA sequence mismatch.";
RL Hum. Mutat. 1:55-62(1992).
RN [25]
RP VARIANT OI-II ASP-670.
RX MEDLINE=93054637; PubMed=1385413;
Query Match 46.8%; Score 184.5; DB 1; Length 1366;
Best Local Similarity 42.9%; Pred. No. 7e-11;
Matches 39; Conservative 9; Mismatches 22; Indels 21; Gaps 2;
Qy 1 GPXGDGEGKDDPGEBCGKGVMPGKIGKBLGDMGRNIGTGPCKX----- 51
Db 559 GPSGPGAGEVKGPEGRHGEFGLPGPGRGERGPGSGAAGTGPIGSRGSGPFGPD 618
Qy 52 GDGGEKGLL-----GIPGEGKAG 70
Db 619 GNKGEGVGVGAVTACPSGSLPGERGAG 649
RESULT 5
CA2B MOUSE STANDARD; PRT; 1736 AA.
ID CA2B MOUSE
AC Q64739; Q61432; Q921W0;
DT 15-JUL-1998 (Rel. 36, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Collagen alpha 2(XI) chain precursor.
GN COL1A2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX [1]
RP SEQUENCE FROM N.A. (ISOFORM 7).
RC STRAIN=129/SV;
RA Rowen L., Qin S., Madan A., Loretz C., James R., Dors M., Mix L.,
RA Hall J., Lasky S., Hood L.;
RT "Sequence of the mouse major histocompatibility locus class II
RT region.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-1678 FROM N.A. (ISOFORM 7).
RC STRAIN=FVB/N, and 129/SV; TISSUE=Cartilage;
RX MEDLINE=97135795; PubMed=8981332;
RA Vandenberg P., Vuoristo M.M., Ala-Kokko L., Prockop D.J.;
RT "The mouse coll1a2 gene. Some transcripts from the adjacent rxr-beta
RT gene extend into the coll1a2 gene.";
RL Matrix Biol. 15:359-367(1996).
RN [3]
RP SEQUENCE OF 1-624 FROM N.A. (ISOFORMS 1; 2; 3; 4; 5 AND 6).
RC STRAIN=129/SV;
RX MEDLINE=95138212; PubMed=7836472;
RA Tsunaki N., Kimura T.;
RT "Differential expression of an acidic domain in the amino-terminal
RT propeptide of mouse pro-alpha2(XI) collagen by complex alternative
RT splicing.";
RL J. Biol. Chem. 270:2372-2378(1995).
RN [4]
RP SEQUENCE OF 1-8 FROM N.A.
RC STRAIN=129/SV; TISSUE=Liver;
RX MEDLINE=96427460; PubMed=8830784;
RA Tsunaki N., Kimura T., Mateui Y., Ochi T.;
RT "Separable cis-regulatory elements that contribute to tissue- and
RT site-specific alpha 2(XI) collagen gene expression in the embryonic
RT mouse cartilage.";
RL J. Cell Biol. 134:1573-1582(1996).
RN [5]
RP FUNCTION: May play an important role in fibrillogenesis by
RP controlling lateral growth of collagen II fibrils (By similarity).
CC -! SUBUNIT: Trimers composed of three different chains: alpha 1(XI),
CC alpha 2(XI), and alpha 3(XI). Alpha 3(XI) is a post-translational
CC modification of alpha 1(XI). Alpha 1(XI) can also be found instead
CC of alpha 3(XI)=1(I) (By similarity).
CC -! ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=7;
CC Comment=Additional isoforms seem to exist;
CC Name=1; Synonyms=E56789;
CC IsoId=Q64739-2; Sequence=Displayed;
CC Name=2; Synonyms=E5689;
CC IsoId=Q64739-3; Sequence=VSP_007346;
CC Name=3; Synonyms=E5789;
CC IsoId=Q64739-4; Sequence=VSP_007345;
CC Name=4; Synonyms=E569;
CC IsoId=Q64739-5; Sequence=VSP_007346; VSP_007347;
CC Name=5; Synonyms=E589;
CC IsoId=Q64739-6; Sequence=VSP_007345; VSP_007346;
CC Name=6; Synonyms=E59;
CC IsoId=Q64739-7; Sequence=VSP_007345; VSP_007346; VSP_007347;
CC Name=7;
CC IsoId=Q64739-1; Sequence=VSP_007345; VSP_007347;
CC -! PTM: Prolines at the third position of the tripeptide repeating
CC unit (G-X-Y) are hydroxylated in some or all of the chains.
CC -! SIMILARITY: BELONGS TO THE FIBRILLAR CLASS OF COLLAGENS.
CC -! SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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FT DOMAIN 423 518 SRCR.
FT FT DISULFID 446 507 BY SIMILARITY.
FT FT DISULFID 459 517 BY SIMILARITY.
FT FT DISULFID 487 497 BY SIMILARITY.
FT FT CARBOHYD 87 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 138 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 518 AA; 52730 MW; 80957601EAC23637 CRC64;

Query Match 45.9%; Score 181; DB 1; Length 518;
Best Local Similarity 48.6%; Pred. No. 6.1e-11;
Matches 34; Conservative 10; Mismatches 26; Indels 0; Gaps 0;

QY 1 GPKGDDGKDPGEKHKVGMGPKGKIGLGMGRGNIGKTPGKKGDKGKGLL 60
D5 192 GPGGPGSGEAGLQGLTGAPOKQATGAPGPRGKSGKDGILGTGPKGEGHGTGDKGL 251
QY 61 GIPGKKGKAG 70
D5 252 GLPGNKDGMG 261

RESULT 7
OTOL ONCKE STANDARD; PRT; 508 AA.
ID OTOL ONCKE STANDARD; PRT; 2944 AA.
AC P83371;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Otolin-1 precursor.
GN OTOL.
OS Oncorhynchus keta (Chum salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8016;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 26-40 AND 452-482, FUNCTION, AND
RP TISSUE SPECIFICITY.
RX MEDLINE=21845944; PubMed=11856329;
RA Murayama E., Takagi Y., Chira T., Davis J.G., Greene M.I.,
RA Nagasawa H.;
RT "Fish otolith contains a unique structural protein, otolin-1."
RL Eur. J. Biochem. 269:688-696(2002).
CC -!- FUNCTION: May be part of the internal framework of the otolith
CC where it may provide nucleation sites to facilitate
CC calcification.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Selectively expressed in the sacculus where it
CC is localised to the otolith, the gelatinous layer of the otolithic
CC membrane, and part of the transitional epithelium.
CC -!- PTM: N-glycosylated.
CC -!- SIMILARITY: Contains 1 collagenous domain.
CC -!- SIMILARITY: Contains 1 Clq domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB067770; BAB84561.1; -.
CC GO; GO:0005576; C:extracellular; IDA.
CC GO; GO:0045299; P:otolith mineralization; NAS.
CC InterPro; IPR001073; Clq.
CC InterPro; IPR008161; Clq_helix.
CC InterPro; IPR008160; Collagen.
CC InterPro; IPR008983; TNF_like.
CC Pfam; PF00386; Clq; 1.
CC PRINTS; PF01391; Collagen; 4.
CC ProDom; PD000007; COMPLEMENTC1Q.
CC ProDom; PD000007; Clq_helix; 1.
RN [5]
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DR PROSITE; PS01113; Clq; 1.
KW Collagen; Glycoprotein; Signal.
FT SIGNAL 1 25
FT CHAIN 26 508 OTOLIN-1.
FT DOMAIN 144 367 COLLAGEN-LIKE.
FT FT DOMAIN 369 505 Clq.
FT FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 416 416 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 508 AA; 52138 MW; 90438799ACE3E9BE CRC64;

Query Match 45.8%; Score 180.5; DB 1; Length 508;
Best Local Similarity 48.1%; Pred. No. 6.7e-11;
Matches 37; Conservative 11; Mismatches 22; Indels 7; Gaps 2;

QY 1 GPKGDDGKDP-----GEEGKGGKVGMPKGKIGLGMGRGNIGKTPGKKGDK 54
D5 231 GLKGLGGERGKPGWNGTQGEKGLKIGPAGSLGTGPMGQNGKGMGEC-PTGKGEK 289
QY 55 GEKGLGIPGKKGAGT 71
D5 290 GEAGLPGPGRGLVGT 306

RESULT 8
CAL7 HUMAN STANDARD; PRT; 2944 AA.
ID CAL7 HUMAN STANDARD; PRT; 2944 AA.
AC Q02388; Q14054; Q16507;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Collagen alpha 1(VII) chain precursor (Long-chain collagen) (LC
DE collagen).
GN COL7A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94327588; PubMed=8051117;
RA Cristiano A.M., Greenspan D.S., Lee S., Utito J.;
RT "Cloning of human type VII collagen. Complete primary sequence of the
RT alpha 1(VII) chain and identification of intragenic polymorphisms."
RL J. Biol. Chem. 269:20255-20262(1994).
RN [2]
RP SEQUENCE OF 128-1493 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=93338437; PubMed=1307247;
RA Cristiano A.M., Rosenbaum L.M., Chung-Honet L.C., Parente M.G.,
RA Woodley D.T., Pan T.C., Zhang R.Z., Chu M.-L., Burgeson R.E.,
RA Utito J.;
RT "The large non-collagenous domain (NC-1) of type VII collagen is
RT amino-terminal and chimeric. Homology to cartilage matrix protein,
RT the type III domains of fibronectin and the A domains of von
RT Willebrand factor."
RL Hum. Mol. Genet. 1:475-481(1992).
RN [3]
RP SEQUENCE OF 815-1439 FROM N.A.
RX MEDLINE=91334380; PubMed=1871109;
RA Parente M.G., Chung L.C., Ryyanen J., Woodley D.T., Wynn K.W.,
RA Bauer E.A., Mattei M.-G., Chu M.-L., Utito J.;
RT "Human type VII collagen: cDNA cloning and chromosomal mapping of the
RT gene."
RL Proc. Natl. Acad. Sci. U.S.A. 88:6931-6935(1991).
RN [4]
RP SEQUENCE OF 369-1255 FROM N.A.
RX MEDLINE=93107742; PubMed=1469284;
RA Gammon W.R., Abernethy M.L., Padilla K.M., Prisavanh P.S.,
RA Cook M.E., Wright J., Briggaman R.A., Hunt S.W. III;
RT "Noncollagenous (NC1) domain of collagen VII resembles multidomain
RT adhesion proteins involved in tissue-specific organization of
RT extracellular matrix."
RL J. Invest. Dermatol. 99:691-696(1992).
RN [5]
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RP SEQUENCE OF 340-675 FROM N.A.
RC TISSUE=Keratinocytes;
RX MEDLINE=9221902; PubMed=1567409;
RA Tanaka T., Takahashi K., Furukawa F., Imamura S.;
RT "Molecular cloning and characterization of type VII collagen cDNA.";
RL Biochem. Biophys. Res. Commun. 183:958-963(1992).
RN [6]
RP SEQUENCE OF 2395-2944 FROM N.A.
RX MEDLINE=93271985; PubMed=8499916;
RA Greenspan D.S.;
RT "The carboxyl-terminal half of type VII collagen, including the non-collagenous NC-2 domain and intron/exon organization of the corresponding region of the COL7A1 gene.";
RL Hum. Mol. Genet. 2:273-278(1993).
RN [7]
RP SEQUENCE OF 1-87 FROM N.A.
RX TISSUE=Placenta;
RC MEDLINE=94375010; PubMed=8088784;
RA Christiano A.M., Hoffman G.G., Chung-Honet L.C., Lee S., Cheng W.,
RT "Structural organization of the human type VII collagen gene (COL7A1), composed of more exons than any previously characterized gene.";
RL Genomics 21:169-179(1994).
RN [8]
RP VARIANT EBSDC ARG-2034.
RX MEDLINE=89227237; PubMed=2653224;
RA Fine J.D., Johnson L., Wright T.;
RT "Epidermolysis bullosa simplex superficialis. A new variant of epidermolysis bullosa characterized by subcorneal skin cleavage mimicking peeling skin syndrome.";
RL Arch. Dermatol. 125:633-638(1989).
RN [9]
RP REVIEW ON DEB VARIANTS.
RX MEDLINE=98041696; PubMed=9375848;
RA Jaervikallio A., Pulkkinen L., Uitto J.;
RT "Molecular basis of dystrophic epidermolysis bullosa: mutations in the type VII collagen gene (COL7A1).";
RL Hum. Mutat. 10:338-347(1997).
RN [10]
RP VARIANT DEB LYS-2798.
RX MEDLINE=92291877; PubMed=8513326;
RA Christiano A.M., Greenspan D.S., Hoffman G.G., Zhang X., Tamai Y.,
RL Lin A.N., Dietz H.C., Hovnanian A., Uitto J.;
RT "A missense mutation in type VII collagen in two affected siblings with recessive dystrophic epidermolysis bullosa.";
RL Nat. Genet. 4:62-66(1993).
RN [11]
RP VARIANT DEB SER-2040.
RX MEDLINE=94224777; PubMed=8170945;
RA Christiano A.M., Rymnen M., Uitto J.;
RT "Dominant dystrophic epidermolysis bullosa: identification of a Gly--Ser substitution in the triple-helical domain of type VII collagen.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3549-3553(1994).
RN [12]
RP VARIANT DEB CYS-2623.
RX MEDLINE=96081220; PubMed=8541842;
RA Christiano A.M., Lee J.Y., Chen W.J., Laforgia S., Uitto J.;
RT "Pretibial epidermolysis bullosa: genetic linkage to COL7A1 and identification of a glycine-to-cysteine substitution in the triple-helical domain of type VII collagen.";
RL Hum. Mol. Genet. 4:1579-1583(1995).
RN [13]
RP VARIANT DEB ARG-2043.
RX MEDLINE=95164985; PubMed=7861014;
RA Christiano A.M., Morriconi A., Faradisi M., Angelo C., Mazzanti C.,
RA Cavallieri R., Uitto J.;
RT "A glycine-to-arginine substitution in the triple-helical domain of type VII collagen in a family with dominant dystrophic epidermolysis bullosa.";
RL J. Invest. Dermatol. 104:438-440(1995).
RN [14]
RP VARIANTS DEB.
RX MEDLINE=98410969; PubMed=9740253;
RA Kon A., Pulkkinen L., Ishida-Yamamoto A., Hashimoto I., Uitto J.;
RT "Novel COL7A1 mutations in dystrophic forms of epidermolysis

RX MEDLINE=96220218; PubMed=8644729;
RA Christiano A.M., McGrath J.A., Tan K.C., Uitto J.;
RT "Glycine substitutions in the triple-helical region of type VII collagen result in a spectrum of dystrophic epidermolysis bullosa phenotypes and patterns of inheritance.";
RL Am. J. Hum. Genet. 58:671-681(1996).
RN [15]
RP VARIANT DEB ARG-2575.
RX MEDLINE=96154068; PubMed=8592061;
RA Shimizu H., McGrath J.A., Christiano A.M., Nishikawa T., Uitto J.;
RT "Molecular basis of recessive dystrophic epidermolysis bullosa: genotype/phenotype correlation in a case of moderate clinical severity.";
RL J. Invest. Dermatol. 106:119-124(1996).
RN [16]
RP VARIANT DEB ARG-1782.
RX MEDLINE=96183562; PubMed=8618018;
RA Christiano A.M., McGrath J.A., Uitto J.;
RT "Influence of the second COL7A1 mutation in determining the phenotypic severity of recessive dystrophic epidermolysis bullosa.";
RL J. Invest. Dermatol. 106:766-770(1996).
RN [17]
RP VARIANT DEB ASP-2073.
RX MEDLINE=96310789; PubMed=8757758;
RA Dunnill M.G.S., McGrath J.A., Richards A.J., Christiano A.M.,
RT Uitto J., Pope F.M., Eady R.A.J.;
RT "Clinicopathological correlations of compound heterozygous COL7A1 mutations in recessive dystrophic epidermolysis bullosa.";
RL J. Invest. Dermatol. 107:171-177(1996).
RN [18]
RP VARIANTS DEB TRP-1982; GLY-2008; ALA-2025; GLU-2049; TRP-2063 AND ARG-2575.
RX MEDLINE=97465605; PubMed=9326325;
RA Hovnanian A., Rochat A., Bodemer C., Petit E., Rivers C.A., Prost C.,
RA Fraitag S., Christiano A.M., Uitto J., Lathrop M., Barrandon Y.,
RA de Prost Y.;
RT "Characterization of 18 new mutations in COL7A1 in recessive dystrophic epidermolysis bullosa provides evidence for distinct molecular mechanisms underlying defective anchoring fibril formation.";
RL Am. J. Hum. Genet. 61:599-610(1997).
RN [19]
RP VARIANT DEB ARG-1652.
RX MEDLINE=98106792; PubMed=9444387;
RA Cserhalmi-Friedman P.B., Karpatis S., Horvath A., Christiano A.M.;
RT "Identification of a glycine substitution and a splice site mutation in the type VII collagen gene in a proband with mitis recessive dystrophic epidermolysis bullosa.";
RL Arch. Dermatol. Res. 289:640-645(1997).
RN [20]
RP VARIANTS DEB ARG-2009 AND ARG-2043.
RX MEDLINE=97358588; PubMed=9215684;
RA Winberg J.-O., Hammami-Hausali N., Nilsson O., Anton-Lamprecht I.,
RA Naylor S.L., Kerbacher K., Zimmermann M., Krajci P.,
RA Gedde-Dahl T., Jr., Bruckner-Tuderman L.;
RT "Modulation of disease severity of dystrophic epidermolysis bullosa by a splice site mutation in combination with a missense mutation in the COL7A1 gene.";
RL Hum. Mol. Genet. 6:1125-1135(1997).
RN [21]
RP VARIANTS DEB ASP-1519; ASP-2006; GLU-2015 AND ARG-2034.
RX MEDLINE=98334662; PubMed=9668111;
RA Hammami-Hausali N., Schumann H., Raghunath M., Kilgus O., Luethi U.,
RA Lager T., Bruckner-Tuderman L.;
RT "Some, but not all, glycine substitution mutations in COL7A1 result in intracellular accumulation of collagen VII, loss of anchoring fibrils, and skin blistering.";
RL J. Biol. Chem. 273:19228-19234(1998).
RN [22]
RP VARIANTS DEB CYS-2008; ARG-2207 AND SER-2775.
RX MEDLINE=98410969; PubMed=9740253;
RA Kon A., Pulkkinen L., Ishida-Yamamoto A., Hashimoto I., Uitto J.;
RT "Novel COL7A1 mutations in dystrophic forms of epidermolysis

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RT bullosa."
RL J. Invest. Dermatol. 111:534-537(1998).
RN [23]
RP VARIANT DB ARG-1347.
RX MEDLINE=90019477; PubMed=9804332;
RA Terracina M., Posteraro P., Schubert M., Sonogo G., Atzori F.,
Query Match 45.6%; Score 179.5; DB 1; Length 2944;
Best Local Similarity 43.4%; Pred. No. 4.6e-10;
Matches 36; Conservative 11; Mismatches 23; Indels 13; Gaps 1;
Qy 1 GPKGDDEKGPGEKGKHKVGMGKGIKGLGDMGRGNIGKTCG----- 47
Db 1667 GPVGEKDDQDGDGDRGDRGSPGSGPKGRGEPGPGPGLVDTGPGAREKGEPGDRGQ 1726
Qy 48 IGKKGDKGEGGLGIGPKGKAG 70
Db 1727 EGPRGPKGDPGLPGAGERGIEG 1749
RESULT 9
CA16 HUMAN
ID CA16 HUMAN STANDARD; PRT; 1028 AA.
AC P12109; O00117; O01118; Q14040; Q14041; Q16258;
DT 01-OCT-1989 (Rel. 12, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Collagen alpha 1(VI) chain precursor.
GN COL6A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=90053396; PubMed=2551669;
RA Chu M.-L., Pan T.-C., Conway D., Kuo H.-J., Glanville R.W., Timpl R.,
Mann K., Deutzmann R.;
RT "Sequence analysis of alpha 1(VI) and alpha 2(VI) chains of human type
VI collagen reveals internal triplication of globular domains similar
to the A domains of von Willebrand factor and two alpha 2(VI) chain
variants that differ in the carboxy terminus."
RL EMBO J. 8:1939-1946(1989).
RN [2]
RP SEQUENCE OF 144-268 AND 593-1028 FROM N.A.
RX MEDLINE=97262101; PubMed=9107679;
RA Trikka D., Davis T., Lapenta V., Brahe C., Kessling A.M.;
RT "Human COL6A1: Genomic characterization of the globular domains,
structural and evolutionary comparison with COL6A2."
RL Mamm. Genome 8:342-345(1997).
RN [3]
RP SEQUENCE OF 257-592 FROM N.A.
RX MEDLINE=89066644; PubMed=3198591;
RA Chu M.-L., Conway D., Pan T.-C., Baldwin C., Mann K., Deutzmann R.,
Timpl R.;
RT "Amino acid sequence of the triple-helical domain of human collagen
type VI."
RL J. Biol. Chem. 263:18601-18606(1988).
RN [4]
RP SEQUENCE OF 287-592 FROM N.A.
RX MEDLINE=92112205; PubMed=1745372;
RA Saitta B., Wang Y.-M., Renkart L., Zhang R.-Z., Pan T.-C., Timpl R.,
Chu M.-L.;
RT "The exon organization of the triple-helical coding regions of the
human alpha 1(VI) and alpha 2(VI) collagen genes is highly similar."
RL Genomics 11:145-153(1991).
RN [5]
RP SEQUENCE OF 422-492 FROM N.A.
RX MEDLINE=88029444; PubMed=365927;
RA Chu M.-L., Mann K., Deutzmann R., Pribula-Conway D.,
Hsu-Chen C.-C., Bernard M.P., Timpl R.;
RT "Characterization of three constituent chains of collagen type VI by

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peptide sequences and cDNA clones."
RL Eur. J. Biochem. 168:309-317(1987).
RN [6]
RP SEQUENCE OF 422-482 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=88161046; PubMed=3348212;
RA Weil D., Mattei M.-G., Passage E., N'Guyen V.C., Pribula-Conway D.,
Mann K., Deutzmann R., Timpl R., Chu M.-L.;
RT "Cloning and chromosomal localization of human genes encoding the
three chains of type VI collagen."
RL Am. J. Hum. Genet. 42:435-445(1988).
RN [7]
RP SEQUENCE OF 1-380 AND 383-1028 FROM N.A.
RX MEDLINE=94222059; PubMed=8168508;
RA Tillot E., Wiedemann H., Golbik R., Pan T.-C., Zhang R.-Z., Mann K.,
Chu M.-L., Timpl R.;
RT "Recombinant expression and structural and binding properties of
alpha 1(VI) and alpha 2(VI) chains of human collagen type VI."
RL Eur. J. Biochem. 221:177-185(1994).
RN [8]
RP VARIANT BM VAL-305.
RX MEDLINE=96376983; PubMed=8782832;
RA Joeblis G.J., Keizers H., Vreijling J.P., de Visser M., Speer M.C.,
Wolterman R.A., Baas F., Bohlhuis P.A.;
RT "Type VI collagen mutations in Bethlem myopathy, an autosomal dominant
myopathy with contractures."
RL Nat. Genet. 14:113-115(1996).
RN [9]
RP VARIANTS BM ARG-121 AND ASP-341.
RX MEDLINE=21853823; PubMed=11865138;
RA Scacheri P.C., Gallanders E.M., Subramony S.H., Vedanarayanan V.,
Crowe C.A., Thakore N., Bingler M., Hoffman E.P.;
RT "Novel mutations in collagen VI genes: expansion of the Bethlem
myopathy phenotype."
RL Neurology 58:593-602(2002).
CC -!- FUNCTION: Collagen VI acts as a cell-binding protein.
CC -!- SUBUNIT: Trimers composed of three different chains: alpha 1(VI),
alpha 2(VI), and alpha 3(VI).
CC -!- PTM: Prolines at the third position of the tripeptide repeating
unit (G-X-Y) are hydroxylated in some or all of the chains.
CC -!- DISEAS: Defects in COL6A1 are a cause of Bethlem myopathy (BM)
[MIM:158810]. BM is a rare autosomal dominant proximal myopathy
characterized by early childhood onset (complete penetrance by the
age of 5) and joint contractures most frequently affecting the
elbows and ankles.
CC -!- SIMILARITY: Contains 3 VWFA domains.
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or send an email to license@isb-sib.ch).
CC EMBL; X15879; CAA33888.1; -
CC EMBL; X15880; CAA33889.1; -
CC EMBL; S75420; AAB20835.2; -
CC EMBL; S75385; AAB20835.2; JOINED.
CC EMBL; S75388; AAB20835.2; JOINED.
CC EMBL; S75390; AAB20835.2; JOINED.
CC EMBL; S75392; AAB20835.2; JOINED.
CC EMBL; S75394; AAB20835.2; JOINED.
CC EMBL; S75396; AAB20835.2; JOINED.
CC EMBL; S75398; AAB20835.2; JOINED.
CC EMBL; S75400; AAB20835.2; JOINED.
CC EMBL; S75402; AAB20835.2; JOINED.
CC EMBL; S75404; AAB20835.2; JOINED.
CC EMBL; S75406; AAB20835.2; JOINED.
CC EMBL; S75408; AAB20835.2; JOINED.
CC EMBL; S75410; AAB20835.2; JOINED.
CC EMBL; S75412; AAB20835.2; JOINED.
CC EMBL; S75414; AAB20835.2; JOINED.

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DR EMBL; S75416; AAB20835.2; JOINED.
DR EMBL; S75418; AAB20835.2; JOINED.
DR EMBL; X99109; CAA67559.1; -.
DR EMBL; X99135; CAA67576.1; -.
DR EMBL; X99136; CAA67576.1; JOINED.
DR EMBL; X06194; CAA29555.1; -.
DR EMBL; M20776; -. NOT ANNOTATED_CDS.
DR EMBL; M27447; AAB52055.1; -.
DR PIR; S05377; CGHUIA.
DR Genew; HGNC:2211; COL6A1.
DR MIM; 120220; -.
DR MIM; 158810; -.
DR GO; GO:0005589; C:collagen type VI; NAS.
DR GO; GO:0007155; P:cell adhesion; NAS.
DR InterPro; IPR008161; Clg_helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF01391; Collagen; 4.
DR Pfam; PF00092; vwa; 3.
DR PRINTS; PR00453; VWFADOMAIN.
DR PRODOM; PDC000007; Clg_helix; 3.
DR SMART; SM00327; VWA; 3.
DR PROSITE; PS0234; VWFA; 3.
KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW Glycoprotein; Collagen; Cell adhesion; Signal; Disease mutation.
FT SIGNAL 1 19
FT CHAIN 20 1028
FT DOMAIN 20 256
FT DOMAIN 257 592
FT DOMAIN 593 1028
FT DOMAIN 37 235
FT DOMAIN 615 805
FT DOMAIN 829 1021
FT SITE 262 264
FT SITE 442 444
FT SITE 478 480
FT CARBOHYD 212 212
FT CARBOHYD 516 516
FT CARBOHYD 537 537
FT CARBOHYD 804 804
FT CARBOHYD 896 896
FT VARIANT 121 121
FT VARIANT 305 305
FT VARIANT 341 341
FT CONFLICT 438 438
FT SEQUENCE 1028 AA; 108547 MW; 3D6CCD9A74146D0E CRC64;
Query Match 45.4%; Score 179; DB 1; Length 1028;
Best Local Similarity 44.0%; Pred. No. 1.9e-10;
Matches 37; Conservative 11; Mismatches 24; Indels 12; Gaps 2;
QY 1 GPKGDD---GSKGDFGEGKHGKVGVRGPKGKGELGDMGRGNIGKTGPIGKKGDKGK 56
Db 389 GPGSDGEPGAPGPPGKGEAGDEGPGDPCGGERGPGGPRGTGPGPRGDPGGA 448
QY 57 -----KGLLGIPGEGKAGTV 72
Db 449 GPGDQDQREGPVGVGDPGEAGPI 472
RESULT 10
COT7 HUMAN
ID COT7 HUMAN STANDARD; PRT; 289 AA.
AC Q9BXJ2.
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Complement-clg tumor necrosis factor-related protein 7 precursor.
GN C1QTNF7 OR CTRP7.
OS Homo sapiens (Human).
```

Db 119 GPGPKGDRG 128

RESULT 11

CALA CHICK
 ID CA1A_CHICK STANDARD; PRT; 674 AA.
 AC P08125;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE collagen alpha 1(X) chain precursor.
 GN COL10A1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE OF 48-674 FROM N.A., AND SEQUENCE OF 103-117 AND 453-466.
 RX MEDLINE=86168227; PubMed=3082876;
 RA Nimomiya Y., Gordon M., van der Rest M., Schmid T., Linsenmayer T.,
 Olsen B.R.;
 RT "The developmentally regulated type X collagen gene contains a long
 open reading frame without introns.";
 RL J. Biol. Chem. 261:5041-5050(1986).
 RN [2]
 RP SEQUENCE OF 1-75 FROM N.A.
 RX MEDLINE=89054019; PubMed=2461368;
 RA Luvall P., Nimomiya Y., Rosenblum N.D., Olsen B.R.;
 RT "The type X collagen gene. Intron sequences split the 5'-untranslated
 region and separate the coding regions for the non-collagenous amino-
 terminal and triple-helical domains.";
 RL J. Biol. Chem. 263:18378-18385(1988).
 RN [3]
 RP REVISIONS TO C-TERMINUS.
 RX MEDLINE=89380199; PubMed=2476437;
 RA Yamaguchi N., Benva P.D., van der Rest M., Nimomiya Y.;
 RT "The cloning and sequencing of alpha 1(VIII) collagen cDNAs
 demonstrate that type VIII collagen is a short chain collagen and
 contains triple-helical and carboxyl-terminal non-triple-helical
 domains similar to those of type X collagen.";
 RL J. Biol. Chem. 264:16022-16029(1989).
 CC -1- FUNCTION: Type X collagen is a product of hypertrophic
 chondrocytes and has been localized to presumptive
 mineralization zones of hyaline cartilage.
 CC -1- SUBUNIT: Homotrimer.
 CC -1- PM: Prolines at the third position of the tripeptide repeating
 unit (G-X-Y) are hydroxylated in some or all of the chains.
 CC -1- SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.
 CC -1- SIMILARITY: Contains 1 C1Q domain.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M13496; AAA48736.1; ALT_SEQ.
 DR EMBL; J04194; AAA48634.1; -.
 DR PIR; S23297; S23297.
 DR InterPro; IPR001073; C1q.
 DR InterPro; IPR008161; C1q helix.
 DR InterPro; IPR008160; Collagen.
 DR InterPro; IPR008983; TNF_like.
 DR Pfam; PF00386; C1q; 1.
 DR Pfam; PF01391; Collagen; 8.
 DR PRINTS; PR00007; COMPLEMENTC1Q.
 DR ProDom; PD000007; C1q helix; 1.
 DR SMART; SM00110; C1q; 1.
 DR PROSITE; PS01113; C1Q; 1.
 KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;

KW Collagen; Signal. 18
 FT SIGNAL 19 674
 FT CHAIN 19 52
 FT DOMAIN 53 512
 FT DOMAIN 53 512
 FT DOMAIN 539 674
 FT DOMAIN 539 674
 FT MOD_RES 453 453
 FT MOD_RES 453 456
 FT MOD_RES 456 456
 SQ SEQUENCE 674 AA; 66434 MW; EAB48B1EF174B145 CRC64;
 Query Match 45.3%; Score 178.5; DB 1; Length 674;
 Best Local Similarity 49.4%; Pred. No. 1.4e-10;
 Matches 39; Conservative 8; Mismatches 23; Indels 9; Gaps 2;
 QY 1 GPKGDDGKGPGEKKGKVGKRMGPKGIK---CSFLGDMGDRGNIGKTGPIGKKGKGEK 57
 DB 313 GPKGDDGKGPGEKKGKVGKRMGPKGIK---CSFLGDMGDRGNIGKTGPIGKKGKGEK 57
 QY 58 GLLGI-----PGKKGKAG 70
 DB 373 GLPGLDGKPGYFGKQLPG 391
 RESULT 12
 CA21_CHICK
 ID CA21_CHICK STANDARD; PRT; 1362 AA.
 AC P02467; P87491; P87492; Q90758; Q90792; Q90795; Q90797; Q92014;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Collagen alpha 2(I) chain precursor (Fragments).
 GN COL1A2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE OF 1-245; 262-448 AND 466-1362 FROM N.A.
 RX MEDLINE=86185168; PubMed=3868961;
 RA Boedtker H., Finer M., Aho S.;
 RT "The structure of the chicken alpha 2 collagen gene.";
 RL Ann. N.Y. Acad. Sci. 460:85-116(1985).
 RN [2]
 RP SEQUENCE OF 1-89 FROM N.A.
 RX MEDLINE=83246518; PubMed=6135195;
 RA Tate V.E., Finer M.H., Boedtker H., Doty P.;
 RT "Chick pro alpha 2 (I) collagen gene: exon location and coding
 potential for the prepropeptide.";
 RL Nucleic Acids Res. 11:91-104(1983).
 RN [3]
 RP SEQUENCE OF 1-14 FROM N.A.
 RX MEDLINE=82060240; PubMed=6946474;
 RA Vogeli G., Ohkubo H., Sobel M.E., Yamada Y., Pastan I.,
 de Crombrughe B.;
 RT "Structure of the promoter for chicken alpha 2 type I collagen gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:5334-5338(1981).
 RN [4]
 RP SEQUENCE OF 1-33 FROM N.A.
 RX MEDLINE=84297217; PubMed=6473103;
 RA Aho S., Tate V.E., Boedtker H.;
 RT "Location of the 11 bp exon in the chicken pro alpha 2(I) collagen
 gene.";
 RL Nucleic Acids Res. 12:6117-6125(1984).
 RN [5]
 RP SEQUENCE OF 1-79 FROM N.A.
 RX MEDLINE=88056316; PubMed=3678834;
 RA Finer M.H., Boedtker H., Doty P.;
 RT "Construction and characterization of cDNA clones encoding the 5' end
 of the chicken pro alpha 1(I) collagen mRNA.";
 RL Gene 56:71-78(1987).
 RN [6]


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DR InterPro; IPR008160; Collagen.
DR InterPro; IPR008885; Fib collagen C.
DR ProDom; PD000007; Clg helix; 4.
DR ProDom; PD002078; Fib collagen_C; 1.
DR SMART; SN00038; COLF1; 1.
KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW Glycoprotein; Collagen; Signal.

Query Match 45.1%; Score 177.5; DB 1; Length 1362;
Best Local Similarity 42.9%; Pred. No. 3.5e-10;
Matches 39; Conservative 8; Mismatches 23; Indels 21; Gaps 2;

QY 1 GPKGDDGKGDGGEKGVKGMGPKIKYKGLGMDGRNIGTKGPKGK----- 51
Db 557 GPGSPAGEAGKFGGKGLHGFVPGPGRGRLPGESGAVGPGPTGSRGSPGPGPD 616
QY 52 GDKGKGLL-----GIPGKKGKAG 70
Db 617 GNKGFGNVGPGAGPAGPAGPGGIPGPGVAG 647

RESULT 13
CA16 CHICK STANDARD; PRT; 1019 AA.
AC P20755;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Collagen alpha 1(VI) chain precursor.
GN COL6A1.
OC Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92241293; PubMed=1572359;
RA Walchli C., Koller E., Trueb J., Trueb B.;
RT "Structural comparison of the chicken genes for alpha 1(VI) and alpha
RT 2(VI) collagen.";
RL Eur. J. Biochem. 205:583-589(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89174602; PubMed=2784434;
RA Bonaldo P., Russo V., Bucciotti F., Bressan G.M., Colombatti A.;
RT "Alpha 1 chain of chick type VI collagen. The complete cDNA sequence
RT reveals a hybrid molecule made of one short collagen and three von
RT Willebrand factor type A-like domains.";
RL J. Biol. Chem. 264:5575-5580(1989).
RN [3]
RP SEQUENCE OF 1-75 FROM N.A.
RX MEDLINE=93011107; PubMed=1396681;
RA Koller E., Trueb B.;
RT "Characterization of the chicken alpha 1(VI) collagen promoter.";
RL Eur. J. Biochem. 208:769-774(1992).
CC -1- FUNCTION: Collagen VI acts as a cell-binding protein.
CC -1- SUBUNIT: Trimers composed of three different chains: alpha 1(VI),
CC alpha 2(VI), and alpha 3(VI).
CC -1- PTM: Prolines at the third position of the tripeptide repeating
CC unit (G-X-Y) are hydroxylated in some or all of the chains.
CC -1- SIMILARITY: Contains 3 WFPA domains.
CC
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CC
DR EMBL; X64458; CAA41062.1; -.
DR EMBL; X57998; CAA41062.1; -.

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DR EMBL; J04598; AAB59954.1; -.
DR EMBL; X57987; CAA41053.1; -.
DR PIR; A32856; A32856.
DR InterPro; IPR008161; Clg helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR002035; VWF A.
DR Pfam; PF01391; Collagen; 6.
DR Pfam; PF00092; vwa; 3.
DR PRINTS; PR00453; VWFADOMAIN.
DR ProDom; PD000007; Clg helix; 3.
DR SMART; SM00327; VWA; 3.
DR PROSITE; PS02334; WFPA; 3.
KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW Glycoprotein; Collagen; Cell adhesion; Signal.
FT SIGNAL 1 19
FT CHAIN 20 1019 COLLAGEN ALPHA 1(VI) CHAIN.
FT DOMAIN 37 233 WFPA 1.
FT DOMAIN 613 800 WFPA 2.
FT DOMAIN 824 1012 WFPA 3.
FT SITE 476 478 CELL ATTACHMENT SITE.
FT SITE 529 531 CELL ATTACHMENT SITE.
FT CARBOHYD 212 212 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 514 514 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 535 535 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 739 739 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 887 887 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1019 AA; 107984 MW; 66E4C334B83BBA21 CRC64;

Query Match 44.8%; Score 176.5; DB 1; Length 1019;
Best Local Similarity 44.0%; Pred. No. 3.3e-10;
Matches 37; Conservative 8; Mismatches 24; Indels 15; Gaps 1;

QY 2 PKGDDGKGDGGEKGVKGMGPKIKYKGLGMDGRNIGTKG 46
Db 253 PRGPGPGDFGEGEGKPKGLPQKGDAGDPGRPGMDGPGVYQGMKGDKSGRSG 312
QY 47 PIKKGDKGKGLLGPCKGKAG 70
Db 313 AKGAKGKKGKIDGIDGMKGEAG 336

RESULT 14
CA21 BOVIN STANDARD; PRT; 1364 AA.
ID CA21 BOVIN
AC P02465; O62649;
DT 21-JUL-1986 (Rel. 01, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Collagen alpha 2(I) chain precursor.
GN COL1A2.
OC Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98290219; PubMed=9628255;
RA Shirai T., Hattori S., Sakaguchi M., Inouye S., Kimura A., Ebihara T.,
RA Irie S., Nagai Y., Horii H.;
RT "The complete cDNA coding sequence for the bovine proalpha2(I) chain
RT of type I procollagen.";
RL Matrix Biol. 17:85-88(1998).
RN [2]
RP SEQUENCE OF 80-98.
RX TISSUE=Skin;
RX MEDLINE=75036115; PubMed=4609475;
RA Fietzek P.F., Breitkreutz D., Kuehn K.;
RT "Amino acid sequence of the amino-terminal region of calf skin
RT collagen.";
RL Biochim. Biophys. Acta 365:305-310(1974).
RN [3]

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SEQUENCE OF 95-415, AND REVISION.
TISSUE=Skin;
RX MEDLINE=76091874; PubMed=173531;
RA Fietzek P.P., Rexrodt F.W.;
RT "The covalent structure of collagen. The amino-acid sequence of
alpha2-CB4 from calf-skin collagen.";
RL Eur. J. Biochem. 59:113-118(1975).
RN [4]
RN SEQUENCE OF 416-445.
RP TISSUE=Skin;
RX MEDLINE=75008198; PubMed=4412523;
RA Fietzek P.P., Furthmayr H., Kuehn K.;
RT "Comparative sequence studies on alpha2-CB2 from calf, human, rabbit
and pig-skin collagen.";
RL Eur. J. Biochem. 47:257-261(1974).
RN [5]
RN SEQUENCE OF 446-481.
RP TISSUE=Skin;
RX MEDLINE=75059250; PubMed=4435743;
RA Fietzek P.P., Kuehn K.;
RT "The covalent structure of collagen: amino acid sequence of the N-
terminal region of alpha2-CB3 from rat skin collagen and alpha2-CB3.5
from calf skin collagen.";
RL Hoppe-Seyler's Z. Physiol. Chem. 355:647-650(1974).
CC -!- FUNCTION: Type I collagen is a member of group I collagen
(fibrillar forming collagen).
CC -!- SUBUNIT: Trimer of one alpha 2(I) and two alpha 1(I) chains.
CC -!- TISSUE SPECIFICITY: Forms the fibrils of tendon, ligaments and
bones. In bones the fibrils are mineralized with calcium
hydroxyapatite.
CC -!- PM: Prolines at the third position of the tripeptide repeating
unit (G-X-Y) are hydroxylated in some or all of the chains.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; AB008683; BAA25171.1; --
DR InterPro; IPR008161; Clg_helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR008085; Fib_collagen_C.
DR Pfam; PF01410; Colf1; 1.
DR ProDom; PD000007; Clg_helix; 3.
DR ProDom; PD002078; Fib_collagen_C; 1.
DR SMART; SW00038; COLFIT 1.
KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW Collagen; Signal; Pyrrolidone carboxylic acid.
FT SIGNAL 1 24 POTENTIAL.
FT PROPEP 25 79 AMINO-TERMINAL PROPEPTIDE.
FT CHAIN 80 1100 COLLAGEN ALPHA 2(I) CHAIN.
FT PROPEP 1101 1364 CARBOXYL-TERMINAL PROPEPTIDE.
FT MOD_RES 80 80 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 84 84 CONVERTED TO AN ALDEHYDE GROUP THAT IS
INVOLVED IN CROSS-LINKING (PROBABLE).
FT MOD_RES 175 175 HYDROXYLATION (PROBABLE).
FT MOD_RES 196 196 HYDROXYLATION (PROBABLE).
FT MOD_RES 262 262 HYDROXYLATION (PROBABLE).
FT MOD_RES 307 307 HYDROXYLATION (PROBABLE).
FT MOD_RES 352 352 HYDROXYLATION (PROBABLE).
FT MOD_RES 157 157 V -> P (IN REF. 3).
FT CONFLICT 187 187 K -> T (IN REF. 3).
FT CONFLICT 211 211 T -> K (IN REF. 3).
FT CONFLICT 298 300 PGA -> AGP (IN REF. 3).
FT CONFLICT 423 424 AT -> TA (IN REF. 4).
SQ SEQUENCE 1364 AA; 129064 MW; 5593FAD6B9ED119A CRC64;

Query Match 44.88; Score 176.5; DB 1; Length 1364;
Best Local Similarity 45.68; Pred. No. 4.3e-10;

Matches 36; Conservative 8; Mismatches 26; Indels 9; Gaps 1;
QY 1 GPKGDDGKGPBEGKHGKVGKMGPKGKGEIGMDGDRGNIGKTGPIGKK----- 51
DB 557 GPAGTAGAGKPGGPGIPGEGFLPGPAGARGGPPGSGAAGTGPIGSRGSPGPPGD 616
QY 52 GDKGEGKGLGIPGEGKAG 70
DB 617 GNGGPGVVGAPGTAGPSG 635
RESULT 15
ID_CALB_MOUSE STANDARD; PRT; 1804 AA.
AC Q61245; Q64047;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Collagen alpha 1(XI) chain precursor.
GN COL11A1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Embryo;
RX MEDLINE=96015067; PubMed=8530046;
RA Yoshioka H., Inoguchi K., Khaleduzzaman M., Ninomiya Y.,
RA Andrikopoulos K., Ramirez P.;
RT "Coding sequence and alternative splicing of the mouse alpha 1(XI)
collagen gene (Col11a1).";
RL Genomics 28:337-340(1995).
RN [2]
RP SEQUENCE OF 181-198 FROM N.A., AND CHONDRODYSPLASIA VARIANT.
RX STRAIN=C57BL/6;
RX MEDLINE=95163095; PubMed=7859283;
RA Li Y., Lacarda D.A., Warman M.L., Beier D.R., Yoshioka H.,
RA Ninomiya Y., Oxford J.T., Morris N.P., Andrikopoulos K.,
RA Ramirez P., Wardell B.B., Liffert G.D., Teuscher C., Woodward S.R.,
RA Taylor B.A., Seegmiller R.B., Olsen B.R.;
RT "A fibrillar collagen gene, Col11a1, is essential for skeletal
morphogenesis.";
RL Cell 80:423-430(1995).
CC -!- FUNCTION: May play an important role in fibrillogenesis by
controlling lateral growth of collagen II fibrils.
CC -!- SUBUNIT: Trimers composed of three different chains: alpha 1(XI),
alpha 2(XI), and alpha 3(XI). Alpha 3(XI) is a post-translational
modification of alpha 1(XI). Alpha 1(XI) can also be found instead
of alpha 3(XI)=1(II) (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long; IsoId=Q61245-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=Q61245-2; Sequence=VSP_001147;
CC -!- PTM: Prolines at the third position of the tripeptide repeating
unit (G-X-Y) are hydroxylated in some or all of the chains.
CC -!- DISEASE: Defects in COL11A1 are associated with chondrodysplasia,
an autosomal recessive disease characterized by skeletal defects
caused by abnormalities in the cartilage of limbs, ribs, mandibles
and trachea.
CC -!- SIMILARITY: BELONGS TO THE FIBRILLAR CLASS OF COLLAGENS.
CC -!- SIMILARITY: HIGH, TO ALPHA 1(V) AND ALPHA 3(V) CHAINS.
CC -!- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
or send an email to license@isb-sib.ch).
CC

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CC EMBL; D38162; BAA07367.1; -
DR EMBL; S74574; AAB33439.1; -
DR PIR; A55648; A55648.
DR MGI; MGI:88446; Coll1a1.
DR InterPro; IPR008161; C1g_helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR008985; ConA_like lec.gl.
DR InterPro; IPR000885; Fib_Collagen_C.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR003129; TSPN.
DR Pfam; PF01410; COLFI; 1.
DR Pfam; PF01391; Collagen; 16.
DR Pfam; PF02210; TSPN; 1.
DR ProDom; PD000007; C1g_helix; 4.
DR ProDom; PD002078; Fib_collagen_C; 1.
DR SMART; SM00038; COLFI; 1.
DR SMART; SM00282; LamG; 1.
DR SMART; SM00210; TSPN; 1.
KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW Glycoprotein; Collagen; Signal; Alternative splicing;
KW Disease mutation.
FT SIGNAL 1 35
FT PROPEP 36 511 AMINO-TERMINAL PROPEPTIDE (POTENTIAL).
FT CHAIN 512 1561 COLLAGEN ALPHA 1(XI) CHAIN.
FT PROPEP 1562 1804 CARBOXYL-TERMINAL PROPEPTIDE.
FT DOMAIN 37 228 TSP N-TERMINAL.
FT DOMAIN 229 417 NONHELICAL REGION.
FT DOMAIN 418 506 TRIPLE-HELICAL REGION (INTERRUPTED).
FT DOMAIN 507 509 SHORT NONHELICAL SEGMENT.
FT DOMAIN 510 527 TELOPEPTIDE.
FT DOMAIN 528 1540 TRIPLE-HELICAL REGION.
FT DOMAIN 1541 1561 NONHELICAL REGION (C-TERMINAL).
FT CARBOHYD 1638 1638 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SITE 610 610 CROSSLINKING.
FT SITE 1450 1450 CROSSLINKING.
FT VARSPLIC 329 413 Missing (in isoform short).
FT VARIANT 189 195 /FTID=VSP_001147.
FT VARIANT 196 1804 LDERSR -> SIEVRDR (IN CHONDRODYSPLASIA).
FT VARIANT 1804 AA; 180963 MW; FE2DB9DEDE1E4219A CRC64;
SQ SEQUENCE 1804 AA; 180963 MW; FE2DB9DEDE1E4219A CRC64;

Query Match 44.8%; Score 176.5; DB 1; Length 1804;
Best Local Similarity 48.1%; Pred. No. 5.7e-10;
Matches 38; Conservative 5; Mismatches 27; Indels 9; Gaps 1;

Qy 1 GPKGDDGKGDGEGKHKGVGR-----MGPKGIKIGELGMDGRGNICKTGPIGKK 51
Db 1079 GPPGPAGKXGAGKGGKGPQGPAGRDVGQGVGLPAGPAGSFGEDGDKGEIGEPGQKSK 1138
Qy 52 GDKGEKGLLGIPGKKGAG 70
Db 1139 GDKGENGPFGPGLQGPVG 1157
```

Search completed: March 8, 2004, 12:12:07
Job time : 12.4185 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:03:01 ; Search time 19.0308 Seconds
(without alignments)
363.925 Million cell updates/sec

Title: US-09-600-932-2_COPY_47_118
Perfect score: 394
Sequence: 1 GPKGDDGKGDPEBEGKHGK.....DKGEKGLGIPGEKKGAGTV 72

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	342	86.8	277	2 JC7903	collectin liver 1
2	205	52.0	645	2 D90782	probable tail fiber
3	205	52.0	645	2 H95612	probable tail fiber
4	196	49.7	618	2 S22436	collagen alpha 2(I)
5	193	49.0	688	2 A53330	collagen alpha 2(I)
6	186.5	47.3	1775	2 A31893	collagen alpha 1(I)
7	184.5	46.8	1366	1 CGRU28	collagen alpha 2(I)
8	184.5	46.8	2551	2 B98047	hypothetical prote
9	183.5	46.6	291	2 T34494	type VII collagen
10	182	46.2	1549	2 I48103	macrophage bacteri
11	181	45.9	518	2 A55840	collagen alpha 2(I)
12	181	45.9	677	2 S23296	collagen alpha 1(X
13	180.5	45.8	674	2 S23297	hypothetical prote
14	180	45.7	181	2 T13518	collagen alpha 1(V
15	179.5	45.6	2944	2 A54849	collagen alpha 1(V
16	179	45.4	438	2 D90734	probable tail fiber
17	179	45.4	1028	1 CGHUIA	collagen alpha 1(V
18	178.5	45.3	1027	2 S28774	collagen alpha cha
19	178	45.2	1146	2 A38587	collagen, cornea-s
20	177.5	45.1	888	2 S28791	collagen alpha 1(X
21	177	44.9	310	2 I50696	collagen alpha 1(I
22	176.5	44.8	1019	1 A32856	collagen alpha 1(V
23	176	44.7	547	2 A36046	collagen alpha cha
24	176	44.7	1532	2 A61262	collagen alpha 1(X
25	175.5	44.5	615	2 A05269	collagen alpha 1(I
26	174.5	44.3	374	1 A42046	surfactant protein
27	174.5	44.3	375	1 A45225	pulmonary surfacta
28	174.5	44.3	1025	2 S34839	collagen alpha 1(V
29	174	44.2	361	2 H90877	probable tail fiber

30	174	44.2	375	2 G85631	hypothetical prote
31	174	44.2	437	2 E90968	probable tail fiber
32	174	44.2	437	2 E90966	probable tail fiber
33	174	44.2	437	2 H90854	probable tail fiber
34	174	44.2	439	2 C90769	probable tail fiber
35	174	44.2	439	2 E85816	probable tail fiber
36	174	44.2	439	2 A85719	probable tail fiber
37	174	44.2	439	2 A85741	hypothetical prote
38	174	44.2	440	2 F85584	probable tail comp
39	174	44.2	920	2 A45748	collagen alpha 1(V
40	174	44.2	1869	1 CGHU4B	collagen alpha 1(I
41	174	44.2	1838	1 CGHUIV	collagen alpha 1(V
42	174	44.2	1843	2 S18803	collagen alpha 1(V
43	173.5	44.0	1496	1 CGHU2V	collagen alpha 2(V
44	173	43.9	358	2 T26281	hypothetical prote
45	173	43.9	1492	2 A40333	collagen alpha 1(V

ALIGNMENTS

RESULT 1
JC7903
collectin liver 1 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 03-Feb-2003 #sequence_revision 03-Feb-2003 #text_change 31-Mar-2003
C/Accession: JC7903
R/Kawai, T.; Suzuki, Y.; Eda, S.; Kase, T.; Ohtani, K.; Sakai, Y.; Keshi, H.; Fukuh, A
Biosci. Biotechnol. Biochem. 66, 2134-2145, 2002
A/Title: Molecular cloning of mouse collectin liver 1.
A/Reference number: JC7903; MUID:22333927; PMID:12450124
A/Accession: JC7903
A/Molecule type: mRNA
A/Residues: 1-277 <KAW>
A/Cross-references: DDBJ:AB016429
A/Experimental source: liver
C/Comment: This protein is a highly conserved cytosolic protein and belongs to a vertebr
c development.
C/Genetics:
A/Gene: Clil
A/Map position: 15

Query Match 86.8%; Score 342; DB 2; Length 277;
Best Local Similarity 86.1%; Pred. No. 2.4e-27;
Matches 62; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 GPKGDDGKGDPEBEGKHGKGVGMGPKGIKGLGDMGDRGNIGKTGPIGKKDKGKGLL 60
DB 47 GPKGDDGGERGDTGEEGKDGKGVKVGQSGKVGKGLGDMGAQGNIGKSGPIGKKDKGKGLL 106
QY 61 GIPGEKKGAGTV 72
DB 107 GIPGEKKGAGTI 118

RESULT 2
D90782
probable tail fiber protein [imported] - Escherichia coli (strain O157:H7, substrain R1
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C/Accession: D90782
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A/Reference number: A99629; MUID:21156231; PMID:11258796
A/Accession: D90782
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-645 <HAY>
A/Cross-references: GB:BA000007; PIDN:BA034651.1; PID:gi3360688; GSPDB:GN00154
A/Experimental source: strain O157:H7, substrain R1MD 0509952
C/Genetics:

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A;Gene: ECs1228
Query Match      52.0%; Score 205; DB 2; Length 645;
Best Local Similarity 54.3%; Pred. No. 3.3e-13;
Matches 38; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 1 GPKGDDGKGDGPGEGKHKVGRMPKGIKGLDMDGRNIGTKTPIGKKGDKGKGLL 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 247 GPGGTGPKGDVGPGRGTGPGVPGQAPGPKGERGDAQAGVAGPAGPRGKGGQGGPGQ 306

QY 61 GIPGKKGKAG 70
    |||:|||||:
Db 307 GIPGLKGDGTG 316

RESULT 3
H85642
probable tail fiber protein Z1483 (similarity) - Escherichia coli (strain O157:H7, subsp
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Nov-2001
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: H85642
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-645 <STO>
A;Cross-references: GB:AE005174; NID:G12514339; PIDN:AGS55604.1; GSPDB:GN00145; UWGP:Z14
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z1483

Query Match      52.0%; Score 205; DB 2; Length 645;
Best Local Similarity 54.3%; Pred. No. 3.3e-13;
Matches 38; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 1 GPKGDDGKGDGPGEGKHKVGRMPKGIKGLDMDGRNIGTKTPIGKKGDKGKGLL 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 247 GPGGTGPKGDVGPGRGTGPGVPGQAPGPKGERGDAQAGVAGPAGPRGKGGQGGPGQ 306

QY 61 GIPGKKGKAG 70
    |||:|||||:
Db 307 GIPGLKGDGTG 316

RESULT 4
S32436
collagen alpha 2(IX) chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Sep-2003
C;Accession: S32436; S34487; S64673
R;Peraelae, M.; Haenninen, M.; Haestbacka, J.; Elima, K.; Vuorio, E.
FEBS Lett. 319, 177-180, 1993
A;Title: Molecular cloning of the human alpha-2(IX) collagen cDNA and assignment of the
A;Reference number: S32436; MUID:93202262; PMID:8454052
A;Accession: S32436
A;Molecule type: mRNA
A;Residues: 1-618 <PER1>
A;Cross-references: EMBL:M95610; NID:G1054872
R;Peraelae, M.; Haenninen, M.; Haestbacka, J.; Vuorio, E.
submitted to the EMBL Data Library, March 1993
A;Description: Molecular cloning of the human alpha-2 (IX) collagen cDNA and assignment
A;Reference number: S34487
A;Accession: S34487
A;Molecule type: mRNA
A;Residues: 1-26 'OT', 29 'S', 31-32 'LM', 35-561 'L', 563-578 'P', 580-618 <PER2>
A;Cross-references: EMBL:M95610; NID:G1054872
R;Diab, M.; Wu, J.J.; Eyre, D.R.
Biochem. J. 314, 327-332, 1996
A;Title: Collagen type IX from human cartilage: a structural profile of intermolecular d
```

```
A;Reference number: S64673; MUID:96195147; PMID:8660302
A;Accession: S64673
A;Molecule type: protein
A;Residues: 123-133 'P', 135-137 <DIA>
A;Comment: Prolines and lysines at the third position of the tripeptide repeating unit
ed and subsequently O-glycosylated.
C;Genetics:
A;Gene: GDB:COL9A2
A;Cross-references: GDB:138310; OMIM:120260
A;Map position: 1p33-1p32.2
A;Complex: type IX collagen may be a heterotrimer of one alpha 1(IX) chain, one alpha 2
C;Function:
A;Description: structural component of extracellular fibrous polymer associated with ty
C;Keywords: chondroitin sulfate proteoglycan; coiled coil; extracellular matrix; glycop.
F11-114/Domain: collagenous COL3 (fragment) #status predicted <NC3>
F115-131/Domain: non-collagenous NC3 #status predicted <NC3>
F132-470/Domain: collagenous COL2 #status predicted <COL2>
F1471-500/Domain: non-collagenous NC2 #status predicted <NC2>
F501-615/Domain: collagenous COL1 #status predicted <COL1>
F616-618/Domain: non-collagenous NC1 (fragment) #status predicted <NC1>
F120/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted
Query Match      49.7%; Score 196; DB 2; Length 618;
Best Local Similarity 51.4%; Pred. No. 2.6e-12;
Matches 36; Conservative 13; Mismatches 21; Indels 0; Gaps 0;

QY 1 GPKGDDGKGDGPGEGKHKVGRMPKGIKGLDMDGRNIGTKTPIGKKGDKGKGLL 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 306 GPGGLPFGSPGPKGEGPGRGIGQGIGKQGDGGERGPGVPGQAPGPKGERGPGQ 365

QY 61 GIPGKKGKAG 70
    |||:|||||:
Db 366 GIPGFGQLPG 375

RESULT 5
A53330
collagen alpha 2(IX) chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 15-Sep-2003
C;Accession: A53330; S22216
R;Peraelae, M.; Elima, K.; Metsaeranta, M.; Rosati, R.; de Crombrughe, B.; Vuorio, E.
J. Biol. Chem. 269, 5064-5071, 1994
A;Title: The exon structure of the mouse alpha2(IX) collagen gene shows unexpected dive
A;Reference number: A53330; MUID:94148964; PMID:8106484
A;Accession: A53330
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-688 <PER>
A;Cross-references: GB:Z22923; NID:G311949; PIDN:CAA80503.1; PID:G311950
R;Elima, K.; Metsaeranta, M.; Kallio, J.; Peraelae, M.; Herola, I.; Garofalo, S.; de Cr
Biochim. Biophys. Acta 1130, 78-80, 1992
A;Title: Specific hybridization probes for mouse alpha-2(IX) and alpha-1(X) collagen mRN
A;Reference number: S22215; MUID:92182017; PMID:1543751
A;Accession: S22216
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 521-524 'M', 526-609 'P', 611-665 'G', 667-668 <ELI>
A;Cross-references: EMBL:X63014; NID:G49810; PIDN:CAA44742.1; PID:G49811
A;Note: the authors translated the codon GAC for residue 526 as His and GGT for residue
C;Genetics:
A;Introns: 24/3; 49/3; 61/3; 82/3; 100/3; 112/3; 120/3; 138/3; 156/3; 172/3; 191/3; 209
/3; 534/1; 597/1; 623/1
C;Keywords: coiled coil; extracellular matrix; glycoprotein; heterotrimer; hydroxylsine
Query Match      49.0%; Score 193; DB 2; Length 688;
Best Local Similarity 45.1%; Pred. No. 5.7e-12;
Matches 37; Conservative 14; Mismatches 19; Indels 12; Gaps 1;

QY 1 GPKGDDGKGDGPGEGKHKVGRMPKGIKGLDMDGRNIGTKTPIGKKGDKGKGLL 48
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 342 GTKGGPKDKGPGQQGLPGVSGPPGKGGEPGRGIGPGQIGMQKGDQGERGPGVPGQ 401
```


A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 58-108 <WEI3>
A;Cross-references: GB:J05049
A;Note: the accession cited by the authors is not found in GenBank
A;Note: parts of this sequence were determined by protein sequencing; a mutant having 93
R;Click, E.M.; Bornstein, P.
Biochemistry 9, 4699-4706, 1970
A;Title: Isolation and characterization of the cyanogen bromide peptides from the alpha
A;Reference number: A90567; MUID:71038625; PMID:5529814
A;Accession: A90567
A;Molecule type: protein
A;Residues: 'Z', '81', 'B', '83-96', '417-447' <CLI>
A;Note: the compositions of peptides CNBR1, CNBR2 were determined; evidence f
P;Kuiyvanemi, H.; Sabol, C.; Tromp, G.; Sippola-Thiele, M.; Prockop, D.J.
J. Biol. Chem. 263, 11407-11413, 1988
A;Title: A 19-base pair deletion in the pro-alpha 2(I) gene of type I procollagen that c
is asymptomatic mother.
A;Reference number: 155264; MUID:88298792; PMID:3403536
A;Accession: 155264
A;Status: translation not shown; translated from GB/EMBL/DBJ
A;Molecule type: DNA; mRNA
A;Residues: 145-197 <KUI2>
A;Cross-references: GB:M21671; NID:G189521; PIDN:AA59994.1; PID:G553506
A;Note: single base mutation in intron leads to abnormal splicing of mRNA
R;Chipman, S.D.; Shapiro, J.R.; McKinstry, M.B.; Stover, M.L.; Branson, P.; Rowe, D.W.
J. Bone Miner. Res. 7, 793-805, 1992
A;Title: Expression of mutant alpha (I)-procollagen in osteoblast and fibroblast culture
A;Reference number: 155485; MUID:92351816; PMID:1642148
A;Accession: 155485
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 163-181, 200-213 <CH2>
A;Cross-references: GB:S41099; NID:G252702; PIDN:AA22761.1; PID:G252703
A;Note: mutant sequence from a patient with osteogenesis imperfecta type IV
R;Moran, P.H.; Jacobs, H.G.; Segrest, J.P.; Cunningham, L.W.
J. Biol. Chem. 245, 5042-5048, 1970
A;Title: Comparative study of glycopeptides derived from selected vertebrate collagens.
A;Reference number: A92069; MUID:71001508; PMID:4319110
A;Accession: B92069
A;Molecule type: protein
A;Residues: 175-180 <MOR>
A;Experimental source: skin
A;Note: attachment of 2-O-alpha-D-glucosyl-O-beta-D-galactose to 5-hydroxylysine
R;Fietzek, P.P.; Furthmayr, H.; Kuehn, K.
Eur. J. Biochem. 47, 257-261, 1974
A;Title: Comparative sequence studies on alpha2-CB2 from calf, human, rabbit and pig-ski
A;Reference number: A91224; MUID:75008198; PMID:4412529
A;Accession: A91224
A;Molecule type: protein
A;Residues: 418-447 <FIE>
R;Tromp, G.; Prockop, D.J.
Proc. Natl. Acad. Sci. U.S.A. 85, 5254-5258, 1988
A;Title: Single base mutation in the pro alpha 2(I) collagen gene that causes efficient
A;Reference number: 159125; MUID:88276936; PMID:2839839
A;Accession: 159125
A;Status: translation not shown; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 520-573 <TRO>
A;Cross-references: GB:M21353; NID:G180881; PIDN:AA52053.1; PID:G180882
A;Note: single base mutation in intron leads to splicing out of exon 28
R;Bernard, M.P.; Myers, J.C.; Chu, M.L.; Ramirez, F.; Eikenberry, E.F.; Prockop, D.J.
Biochemistry 22, 1139-1145, 1983
A;Title: Structure of a cDNA for the proalpha-2 chain of human type I procollagen. Compa
A;Reference number: S09174; MUID:83178919; PMID:6687691
A;Accession: S09174
A;Molecule type: mRNA
A;Residues: 623-742, 'A', 744-764, 'X', 766-827, 'A', 829-830, 'P', 832-836, 'P', 838-1097, 'L', 109
A;Cross-references: GB:J00115; GB:V00503; NID:G30123; PIDN:CAA23761.1; PID:G825646
A;Experimental source: skin fibroblast cells
R;Forlino, A.; Zolezzi, F.; Valli, M.; Pignatti, P.F.; Cetta, G.; Brunelli, P.C.; Motte
Hum. Mol. Genet. 3, 2201-2206, 1994
A;Title: Severe (type III) osteogenesis imperfecta due to glycine substitutions in the
A;Reference number: 154365; MUID:95187161; PMID:7881420
A;Accession: 168663
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 663-675, 'V', 677, 'P', 679-742, 'A', 744-746 <FOR>
A;Cross-references: GB:147668; NID:G1009095; PIDN:AA59577.1; PID:G1009096
R;Niyibizi, C.; Bonadio, J.; Byers, P.H.; Byre, D.R.
J. Biol. Chem. 267, 23108-23112, 1992
A;Title: Incorporation of type I collagen molecules that contain a mutant alpha 2(I) cha
A;Reference number: 155369; MUID:93054637; PMID:1385413
A;Accession: 155369
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 665-666, 'D', 668-670 <NID>
A;Cross-references: GB:100613; NID:G180888; PIDN:AA59384.1; PID:G180889
A;Note: mutant sequence from a patient with osteogenesis imperfecta
R;Bachman, J.F.; Hannagan, M.; Chan, D.; Cole, W.G.
Biochem. J. 276, 765-770, 1991
A;Title: Characterization of a type I collagen alpha 2(I) glycine-586 to valine substit
e method.
A;Reference number: A56799; MUID:91291136; PMID:2064612
A;Accession: A56799
A;Molecule type: mRNA
A;Residues: 672-675, 'V', 677, 'P', 679-681 <BAT>
A;Cross-references: GB:S39878; NID:G1679911; PIDN:AA519314.1; PID:G232761
A;Note: sequence extracted from NCBI backbone (NCBI:39878, NCBI:39886)
A;Note: mutant sequence of patient with osteogenesis imperfecta type IV; the authors su
nrol sequence
R;Maekelae, J.K.; Vuorio, T.; Vuorio, E.
Biochim. Biophys. Acta 1049, 171-176, 1990
A;Title: Growth-dependent modulation of type I collagen production and mRNA levels in c
A;Reference number: S10768; MUID:90304220; PMID:2364107
A;Accession: S10768
A;Molecule type: mRNA
A;Residues: 960-1021, 'L', 1023-1188, 'D', 1190-1197, 'S', 1199-1356 <MAE>
A;Cross-references: EMBL:X55525; NID:G30101; PIDN:CAA39142.1; PID:G30102
A;Experimental source: fibroblast cell culture
R;Myers, J.C.; Chu, M.L.; Faro, S.H.; Clark, W.J.; Prockop, D.J.; Ramirez, F.
Proc. Natl. Acad. Sci. U.S.A. 78, 3516-3520, 1981
A;Title: Cloning a cDNA for the pro-alpha2 chain of human type I collagen.
A;Reference number: A18855; MUID:81273090; PMID:6267597
A;Accession: A18855
A;Molecule type: mRNA
A;Residues: 964-979, 'V', 981-1018, 'Q', 1020 <MYE>
A;Cross-references: GB:J00114; NID:G180393; PIDN:AA51996.1; PID:G180394
A;Note: 1019-Leu was also found
R;Wenstrup, R.J.; Cohn, D.H.; Cohen, T.; Byers, P.H.
J. Biol. Chem. 263, 7734-7740, 1988
A;Title: Arginine for glycine substitution in the triple-helical domain of the products
A;Reference number: 155285; MUID:88227975; PMID:2897363
A;Accession: 155285
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1090-1107 <WEN1>
A;Cross-references: GB:M22816; NID:G179602; PIDN:AA51844.1; PID:G179603
A;Accession: 170059
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1090-1101, 'R', 1103-1107 <WEN2>
A;Cross-references: GB:M22817; NID:G179606; PIDN:AA51846.1; PID:G179607
A;Note: mutant sequence from a patient with osteogenesis imperfecta type IV
R;Myers, J.C.; Dickson, L.A.; de Wet, W.O.; Bernard, M.P.; Chu, M.L.; di Liberto, M.; P
J. Biol. Chem. 258, 10128-10135, 1983
A;Title: Analysis of the 3' end of the human pro-alpha-2(I) collagen gene. Utilization
A;Reference number: S09175; MUID:83290853; PMID:6309769
A;Accession: S09175
A;Molecule type: DNA
Query Match 46.8%; Score 184.5; DB 1; Length 1366;
Best Local Similarity 42.9%; Pred. No. 7.9e-11;
Matches 39; Conservative 9; Mismatches 22; Indels 21; Gaps 2;


```
QY 1 GPKGDDGKGPGEKGGKVGKMGPKIKGELGMDGRGNIGKTGPIGKK----- 51
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 559 GPSGPAEGVGKPGERGLGELFGLPAGPRGPPGESGAAGTGPISGRSGSPGPPGD 618
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 52 GPKGKGLL-----GIPGKKGAG 70
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 619 QNKGPVGVAGTGTAGPSPGSLPGERGAAG 649
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
B98047
hypothetical protein spr1403 [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
C:Accession: B98047
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
y, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: B98047
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2551 <KUR>
A:Cross-references: GB:AE007317; PIDN:AAL00207.1; PID:g15459054; GSPDB:GN00174
C:Genetics:
A:Gene: spr1403

Query Match 46.8%; Score 184.5; DB 2; Length 2551;
Best Local Similarity 52.9%; Pred. No. 1.4e-10;
Matches 37; Conservative 8; Mismatches 22; Indels 3; Gaps 1;

QY 1 GPKGDDGKGPGEKGGKVGKMGPKIKGELGMDGRGNIGKTGPIGKKGKGLL 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1251 GPKGDKGADGAKGKGAQGGRLTGAQGVKGGKDGQGER---GLTSGKGGKGGQGGRLT 1307
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 GIPGKKGAG 70
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1308 GAQGAAGKDGK 1317
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
T34494
hypothetical protein ZK1248.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 15-Sep-2003
C:Accession: T34494
R:Latreille, P.
submitted to the EMBL Data Library, June 1995
A:Description: The sequence of C. elegans cosmid ZK1248.
A:Reference number: Z21534
A:Accession: T34494
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-291 <LAT>
A:Cross-references: EMBL:U29244; PIDN:AACT71083.1; GSPDB:GN00020; CESP:ZK1248.2
A:Experimental source: strain Bristol N2; clone ZK1248
C:Genetics:
A:Gene: CESP:ZK1248.2
A:Map position: 2
A:Introns: 9/3

Query Match 46.6%; Score 183.5; DB 2; Length 291;
Best Local Similarity 45.8%; Pred. No. 2.3e-11;
Matches 38; Conservative 10; Mismatches 22; Indels 13; Gaps 2;

QY 1 GPKGDDGKGPGEKGGKVGKMGPKIKGELGMDGRGNIGKT-----GPI 48
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 183 GPQGPGEKGGKGGADVEH-QVGLPQKISGPTGQGGPQGGTGAQGIAPGGERGR 241
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 49 GKKGDKGKGLLGIIPGKKGAGT 71
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Db 242 GDKDNGNGSAGAPGEGEPGT 264
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
I48103
type VII collagen - Chinese hamster (fragment)
C:Species: Cricetulus griseus (Chinese hamster)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 15-Sep-2003
C:Accession: I48103
R:Greenspan, D.S.
Hum. Mol. Genet. 2, 273-278, 1993
A:Title: The carboxyl-terminal half of type VII collagen, including the non-collagenous
A:Reference number: I48103; MUID:93271985; PMID:8499916
A:Accession: I48103
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1549 <RES>
A:Cross-references: GB:L06863; NID:g388624; PIDN:AAA36968.1; PID:g388625
F:1484-1536/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 46.2%; Score 182; DB 2; Length 1549;
Best Local Similarity 33.3%; Pred. No. 1.6e-10;
Matches 40; Conservative 11; Mismatches 21; Indels 48; Gaps 2;

QY 1 GPKGDD-----GEKGDGPEKGGKVGKMGPKIKGELGMDGRGNIGKTGPIGKKG 52
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1054 GDKDPTGTLPGPRGERGEFDRGEDCHQEQEGRGLMGPPGSRGDRGKGGTGTGAGLKG 1113
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 53 DK-----GEKGLLGIIPGKKGAGTV 72
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1114 DKGDSAVIEGPPGIRGAKGDMGRGPRGIDGDKPRGDNPNPGDKGSGEPGDKGSAGSI 1173
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
A55840
macrophage bacteria-binding receptor MARCO - mouse
C:Species: Mus musculus (house mouse)
C>Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 05-Nov-1999
C:Accession: A55840
R:Elomaa, O.; Kangas, M.; Sahlberg, C.; Tuukkanen, J.; Sormunen, R.; Liakka, A.; Thesle
Cell 80, 603-609, 1995
A:Title: Cloning of a novel bacteria-binding receptor structurally related to scavenger
A:Reference number: A55840; MUID:95171455; PMID:7867067
A:Accession: A55840
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-518 <ELO>
A:Cross-references: GB:U18424; NID:g682722; PIDN:AAA8638.1; PID:g682723
C:Superfamily: scavenger receptor cysteine-rich domain homology
C:Keywords: transmembrane protein
F:418-518/Domain: scavenger receptor cysteine-rich domain homology <SRC>

Query Match 45.9%; Score 181; DB 2; Length 518;
Best Local Similarity 48.6%; Pred. No. 7.1e-11;
Matches 34; Conservative 10; Mismatches 26; Indels 0; Gaps 0;

QY 1 GPKGDDGKGPGEKGGKVGKMGPKIKGELGMDGRGNIGKTGPIGKKGKGLL 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 192 GPQGPQSGKEAGLQGLTGAPKQGGATGAPPRGKSGKGDIGLTGPKGHEGTGKDGDL 251
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 GIPGKKGAG 70
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 252 GLPGNKGDMG 261
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
S23296
collagen alpha 2(IX) chain precursor - chicken
C:Species: Gallus gallus (chicken)
C>Date: 22-Nov-1993 #sequence_revision 09-Mar-1996 #text_change 15-Sep-2003
C:Accession: S23296; C34493; A29032; B29032; B28754; A18856; B18856; A28518; S2;
R:Ninomiya, Y.; Castagnola, P.; Gerecke, D.; Gordon, M.K.; Jacenko, O.; Luvalle, P.; Mc
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maguchi, N.; Olsen, B.R.
in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp.79-114, Academic Press, 1990.
A:Title: The molecular biology of collagens with short triple-helical domains.
A:Reference number: S22243
A:Accession: S23296
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-677 <N1>
R:Nishimura, I.; Muragaki, Y.; Olsen, B.R.
J. Biol. Chem. 264, 20033-20041, 1989
A:Title: Tissue-specific forms of type IX collagen-proteoglycan arise from the use of two promoters.
A:Reference number: A34493; MUID:90062114; PMID:2584206
A:Accession: C34493
A:Molecule type: mRNA
A:Residues: 1-174 <N1>
A:CROSS-references: EMBL:M28660; NID:9211625; PIDN:AAA48709.1; PID:9211626
R:McCormick, D.; van der Rest, M.; Goodship, J.; Lozano, G.; Ninomiya, Y.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 4044-4048, 1987
A:Title: Structure of the glycosaminoglycan domain in the type IX collagen-proteoglycan.
A:Reference number: A29032; MUID:87231947; PMID:3473493
A:Accession: A29032
A:Molecule type: mRNA
A:Residues: 120-195 <MCC>
A:CROSS-references: GB:M16715; NID:9211365; PIDN:AAA48644.1; PID:9555431
A:Accession: E29032
A:Molecule type: protein
A:Residues: 147-165;170-180,'X',182-188 <MC2>
R:Lozano, G.; Olsen, B.R.
submitted to the EMBL Data Library, April 1990
A:Reference number: S22062
A:Accession: S22062
A:Molecule type: DNA
A:Residues: 401,'RA',404-631,'D',633-677 <LO1>
R:Lozano, G.; Ninomiya, Y.; Thompson, H.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 82, 4050-4054, 1985
A:Title: A distinct class of vertebrate collagen genes encodes chicken type IX collagen
A:Reference number: A94705; MUID:85216631; PMID:3858862
A:Accession: B28754
A:Molecule type: DNA
A:Residues: 404-633;644-677 <LO2>
A:CROSS-references: EMBL:M11327
A:Note: this sequence has been revised in reference S22062
R:Ninomiya, Y.; van der Rest, M.; Mayne, R.; Lozano, G.; Olsen, B.R.
Biochemistry 24, 4223-4229, 1985
A:Title: Construction and characterization of cDNA encoding the alpha2 chain of chicken type IX collagen
A:Reference number: A18856; MUID:86026268; PMID:2996593
A:Accession: A18856
A:Molecule type: mRNA
A:Residues: 401,'RA',404-677 <N12>
A:Accession: B18956
A:Molecule type: protein
A:Residues: 433-435,'X',437-450;542-562 <N13>
R:Huber, S.; Winterhalter, K.H.; Vaughan, L.
J. Biol. Chem. 263, 752-756, 1988
A:Title: Isolation and sequence analysis of the glycosaminoglycan attachment site of type IX collagen
A:Reference number: A28518; MUID:88087195; PMID:3335523
A:Accession: A28518
A:Molecule type: protein
A:Residues: 156-159,'X',161-166,'X',168-173,'X',175-178 <HUB>
R:van der Rest, M.; Mayne, R.
J. Biol. Chem. 263, 1615-1618, 1988
A:Title: Type IX collagen proteoglycan from cartilage is covalently cross-linked to type IX collagen
A:Reference number: S23813; MUID:88115274; PMID:3123475
A:Accession: S23813
A:Molecule type: protein
A:Residues: 170-180,'X',182-184 <VAN>
A:Note: evidence for aldimine cross-linkage of 190-lys to collagen alpha 1(III) chain is provided by the structure of type IX collagen.
R:Mayne, R.; van der Rest, M.; Ninomiya, Y.; Olsen, B.R.
Ann. N. Y. Acad. Sci. 460, 38-46, 1985
A:Title: The structure of type IX collagen.
A:Reference number: S22238; MUID:86185164; PMID:3868958
A:Accession: S22238

A:Molecule type: protein
A:Residues: 542-567 <MA>
C:Genetics:
A:Introns: 427/3; 439/3; 454/3; 465/3; 514/3; 533/1; 596/1; 622/1
C:Keywords: chondroitin sulfate proteoglycan; coiled coil; extracellular matrix; glycoprotein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-677/Product: collagen alpha 2(XI) chain #status predicted <MAT>
F:25-161/Domain: non-collagenous COL3 #status predicted <COL3>
F:162-178/Domain: non-collagenous NC3 #status predicted <NC3>
F:179-517/Domain: non-collagenous COL2 #status predicted <COL2>
F:518-547/Domain: non-collagenous NC2 #status predicted <NC2>
F:548-662/Domain: non-collagenous COL1 #status predicted <COL1>
F:663-677/Domain: non-collagenous NC1 #status predicted <NC1>
F:158,178/Modified site: 4-hydroxyproline (Pro) #status experimental
F:167/Binding site: chondroitin sulfate (Ser) (covalent) #status experimental
F:181/Modified site: 5-hydroxylysine (Lys) #status experimental
F:181/Binding site: carbohydrate (Lys) (covalent) #status experimental
F:190/Modified site: allysine (Lys) #status predicted
Query Match 45.9%; Score 181; DB 2; Length 677;
Best Local Similarity 51.3%; Pred. No. 9.1e-11;
Matches 39; Conservative 7; Mismatches 24; Indels 6; Gaps 2;
QY 1 GPKGDCGKGD---PGEKGKGVGRMGPKGIKGL--GDMGDRGNIGKTGPIGKKGDK 54
DB 383 GLKGRGGRGVPVGPAGPGAGSGPGKGGPPGIPQGLPGVKGDKSGPKTGPKGTGDP 442
QY 55 GEKGLGIPGKKGKAG 70
DB 443 GVHGLAGVKKGKGGSG 458
RESULT 13
S23297
collagen alpha 1(X) chain precursor - chicken
N:Alternate names: type X collagen
C:Species: Gallus gallus (chicken)
C:Date: 07-Oct-1994 #sequence revision 10-Nov-1995 #text_change 13-Aug-1999
C:Accession: S23297; A31896; S65594; S77711; I50218
R:Ninomiya, Y.; Castagnola, P.; Gerecke, D.; Gordon, M.K.; Jacenko, O.; Luvalle, P.; Maguchi, N.; Olsen, B.R.
in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp.79-114, Academic Press, 1990.
A:Title: The molecular biology of collagens with short triple-helical domains.
A:Reference number: S22243
A:Accession: S23297
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-674 <N1N>
R:Luvalle, P.; Ninomiya, Y.; Rosenblum, N.D.; Olsen, B.R.
J. Biol. Chem. 263, 18378-18385, 1988
A:Title: The type X collagen gene. Introns sequences split the 5'-untranslated region and the 3'-untranslated region.
A:Reference number: A31896; MUID:89054019; PMID:2461368
A:Accession: A31896
A:Molecule type: mRNA
A:Residues: 1-75 <LUV>
R:Ninomiya, Y.; Gordon, M.; van der Rest, M.; Schmid, T.; Linsemayer, T.; Olsen, B.R.
J. Biol. Chem. 261, 5041-5050, 1986
A:Title: The developmentally regulated type X collagen gene contains a long open reading frame.
A:Reference number: I50218; MUID:86168227; PMID:3082876
A:Accession: S65594
A:Molecule type: DNA
A:Residues: 77,'9','D',11-12,'EOMKLYILFTW',30-31,'TCKSGRAFTTWMILQNMADLVSSHT',48-89,'L',629,'FOAVLSLISMTIKCGSCQIQPMWSIFPLNMFILISQVSLKSNIPITMS' <N1N>
A:CROSS-references: EMBL:M13496; NID:9211699; PIDN:AAA48736.1; PID:9211700
A:Accession: S77711
A:Molecule type: protein
A:Residues: 104-112,'X',114-117;453-466 <N1N2>
C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
C:Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer; hydroxyproline
F:1-18/Domain: signal sequence #status predicted <SIG>
F:547-673/Domain: complement C1q carboxyl-terminal homology <C1Q>
F:453,456/Modified site: hydroxyproline (Pro) #status experimental
F:611/Binding site: carbohydrate (Asn) (covalent) #status predicted

```
Query Match          45.8%; Score 180.5; DB 2; Length 674;
Best Local Similarity 49.4%; Pred. No. 1e-10;
Matches 39; Conservative 8; Mismatches 23; Indels 9; Gaps 2;

QY 1 GPKGDDGKGPGEKGKHKVGRMGPKGK---GELGDMGDRGNIGKTPGKKGKDGKSK 57
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 313 GPKGDDGKGPGEKGKHKVGRMGPKGK---GELGDMGDRGNIGKTPGKKGKDGKSK 57
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 58 GLGK-----GPKGKAG 70
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 373 GLGKDDGKGPGEKGKAG 391
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 14
T13518
hypothetical protein 29 - Bacillus phage phi-105
C:Species: Bacillus phage phi-105
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999
R:Kobayashi, K.; Okamura, K.; Inoue, T.; Sato, T.; Kobayashi, Y.
submitted to the EMBL Data Library, July 1998
A:Description: Complete nucleotide sequence of Bacillus subtilis phage phi-105.
A:Reference number: Z17688
A:Accession: T13518
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-181 <KOB>
A:Cross-references: EMBL:AB016282; NID:d1253051; PID:d1037622; PIDN:BAA36635.1

Query Match          45.7%; Score 180; DB 2; Length 181;
Best Local Similarity 45.8%; Pred. No. 3.3e-11;
Matches 33; Conservative 13; Mismatches 26; Indels 0; Gaps 0;

QY 1 GPKGDDGKGPGEKGKHKVGRMGPKGK---GELGDMGDRGNIGKTPGKKGKDGKSK 60
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 46 GPKGDDGKGPGEKGKHKVGRMGPKGK---GELGDMGDRGNIGKTPGKKGKDGKSK 60
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 61 GPKGDDGKGPGEKGKHKVGRMGPKGK---GELGDMGDRGNIGKTPGKKGKDGKSK 72
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 106 GPKGDDGKGPGEKGKHKVGRMGPKGK---GELGDMGDRGNIGKTPGKKGKDGKSK 117
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 15
A54849
collagen alpha 1(VII) chain precursor - human
N:Alternate names: procollagen alpha 1(VII) chain
C:Species: Homo sapiens (man)
C:Date: 04-Nov-1994 #sequence_revision 04-Nov-1994 #text_change 15-Sep-2003
C:Accession: A54849; PH0844; S16316; I56328; A30296; I84686
R:Christiano, A.M.; Greenspan, D.S.; Lee, S.; Uitto, J.
J. Biol. Chem. 269, 20256-20262, 1994
A:Title: Cloning of human type VII collagen. Complete primary sequence of the alpha1(VII)
A:Reference number: A54849; MUID:94321588; PMID:8051117
A:Accession: A54849
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-2944 <CHR>
A:Cross-references: GB:L02870; NID:9987124; PIDN:AAA75438.1; PID:9987125
R:Tanaka, T.; Takahashi, K.; Furukawa, F.; Imanura, S.
Biochem. Biophys. Res. Commun. 183, 958-963, 1992
A:Title: Molecular cloning and characterization of type VII collagen cDNA.
A:Reference number: PH0844; MUID:92231902; PMID:1567409
A:Accession: PH0844
A:Molecule type: mRNA
A:Residues: 'EPR', 340-475; 'BALSTASHSTLCWRAATRWHPNCRGSHWTRACPCNRPASHRAARAG', 524-528; 'C',
A:Cross-references: DDBJ:D11152; DDBJ:D13694; NID:9453698; PIDN:BA02853.1; PID:9453699
A:Experimental source: keratinocyte
R>Note: the authors translated the codon ACC for residues 394 and 397 as Tyr
A:Parente, M.G.; Chung, L.C.; Ryyanen, J.; Woodley, D.T.; Wynn, K.C.; Bauer, E.A.; Mat
Proc. Natl. Acad. Sci. U.S.A. 88, 6931-6935, 1991
A:Title: Human type VII collagen: cDNA cloning and chromosomal mapping of the gene.
A:Reference number: S16316; MUID:91334380; PMID:1871109
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A:Accession: S16316
A:Molecule type: mRNA
A:Residues: 815-992; 'E', 894-1439 <PAR>
A:Cross-references: GB:M65158; GB:S49017; NID:g180914; PIDN:AAA96439.1; PID:g180915
A:Experimental source: keratinocyte
R:Gammon, W.R.; Abernethy, M.L.; Padilla, K.M.; Prissayanh, P.S.; Cook, M.E.; Wright, J.
J. Invest. Dermatol. 99, 691-696, 1992
A:Title: Noncollagenous (NC1) domain of collagen VII resembles multidomain adhesion pro
A:Reference number: I56328; MUID:93107742; PMID:1469284
A:Accession: I56328
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 'EPR', 372-517; 'DV', 520-540; 'W', 542-1255 <RES>
A:Cross-references: GB:S51236; NID:9262308; PIDN:AB24637.1; PID:9262309
R:Seltzer, J.L.; Eisen, A.Z.; Bauer, E.A.; Morris, N.P.; Glanville, R.W.; Burgeson, R.E
J. Biol. Chem. 264, 3822-3826, 1989
A:Title: Cleavage of type VII collagen by interstitial collagenase and type IV collagen
A:Reference number: A30296; MUID:89139437; PMID:2537292
A:Accession: A30296
A:Molecule type: protein
A:Residues: 'A', 1240-1246; 'G', 1248-1250; 'XE', 1253-1255; 'Q', 1257; 'E', 2032; 'C', 2034-2041;
A>Note: two reported peptides cannot be reliably located
R:Greenspan, D.S.
Hum. Mol. Genet. 2, 273-278, 1993
A:Title: The carboxyl-terminal half of type VII collagen, including the non-collagenous
A:Reference number: I48103; MUID:93271985; PMID:8499916
A:Accession: I48103
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 2395-2871; 'S', 2873-2944 <RE2>
A:Cross-references: GB:I06862; NID:g388713; PIDN:AAA99196.1; PID:g388714
R:Christiano, A.M.; Ryyanen, M.; Uitto, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 3549-3553, 1994
A:Title: Dominant dystrophic epidermolysis bullosa: identification of a Gly --> Ser sub:
A:Reference number: A55255; MUID:94224777; PMID:8170945
A:Contents: annotation
C:Comments: Prolines and lysines at the third position of the tripeptide repeating unit
ed and subsequently O-glycosylated.
C:Genetics:
A:Gene: GDB:COL7A1; EBRI; EBD1; EB
A:Cross-references: GDB:128750; OMIM:120120
A:Map position: 3p21.3-3p21.3
A:Note: defects in this gene can result in dominant and recessive dystrophic epidermoly:
A:Note: there are 118 introns
C:Complex: type VII collagen is probably a homotrimer
C:Function:
A:Description: structural component of extracellular polymer associated with anchoring !
C:Keywords: coiled coil; extracellular matrix; glycoprotein; hydroxylysine; hydroxyprol:
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-2944/Product: collagen alpha 1(VII) chain #status predicted <MAT>
F:17-1253/Domain: amino-terminal nonhelical #status predicted <NC1>
F:36-201/Domain: von Willebrand factor type A repeat homology <VWA1>
F:231-318/Domain: fibronectin type III repeat homology <FN1>
F:327-413/Domain: fibronectin type III repeat homology <FN2>
F:414-502/Domain: fibronectin type III repeat homology <FN3>
F:508-593/Domain: fibronectin type III repeat homology <FN4>
F:598-683/Domain: fibronectin type III repeat homology <FN5>
F:686-771/Domain: fibronectin type III repeat homology <FN6>
F:776-862/Domain: fibronectin type III repeat homology <FN7>
F:864-952/Domain: fibronectin type III repeat homology <FN8>
F:954-1045/Domain: fibronectin type III repeat homology <FN9>
F:1052-1219/Domain: von Willebrand factor type A repeat homology <VWA2>
F:1170-1172/Region: cell attachment (R-G-D) motif
F:1189-1253/Region: cysteine/proline-rich
F:1254-2783/Region: interrupted helical
F:1334-1336/Region: cell attachment (R-G-D) motif
F:2008-2010/Region: cell attachment (R-G-D) motif
F:2553-2555/Region: cell attachment (R-G-D) motif
F:2784-2944/Domain: carboxyl-terminal nonhelical #status predicted <NC2>
F:2876-2923/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:337-786.1109/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:2167.2176, 2185, 2188, 2664, 2667, 2673/Modified site: 4-hydroxyproline (Pro) #status exper
F:2625, 2631/Modified site: 5-hydroxylysine (Lys) #status experimental
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F;2625,2631/binding site: carbohydrate (Lys) (covalent) #status experimental
F;2634,2802,2804/Disulfide bonds: interchain #status predicted

Query Match 45.6%; Score 179.5; DB 2; Length 2944;
Best Local Similarity 43.4%; Pred. No. 5.3e-10;
Matches 36; Conservative 11; Mismatches 23; Indels 13; Gaps 1;

QY 1 GPKGDDGKDPGEGKGVGRMGPKGIKGELGDMGDRGNIGKTGP----- 47
Db 1667 GPVGEKGDQDPGEDGRNGSPGSSGPKGDRGEPPGPPGLVDTGPGAREKGEPPGDRGQ 1726

QY 48 IGGKGDGKGLLIPGEGKAG 70
Db 1727 EGPRGPKGDPGLPGAPGERGIEG 1749

Search completed: March 8, 2004, 12:16:19
Job time : 19.0308 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:07:46 ; Search time 18.7137 seconds
(without alignments)
198.629 Million cell updates/sec

Title: US-09-600-932-2_COPY_47_118
Perfect score: 394
Sequence: 1 GPKGDGEGKDPGEGKHGK.....DKGEGILLGTPGKRGATV 72

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pcp.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pcp.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pcp.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pcp.*
5: /cgn2_6/ptodata/2/iaa/PCPUS_COMB.pcp.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	205	52.0	519	4	US-09-453-702B-265
2	184.5	46.8	1024	3	US-08-931-820-2
3	184.5	46.8	1366	3	US-08-963-825-19
4	184.5	46.8	1366	4	US-09-500-811-19
5	184.5	46.8	1366	4	US-09-570-573-19
6	184.5	46.8	1366	4	US-09-548-608-19
7	184.5	46.8	1366	4	US-09-585-887-10
8	184.5	46.8	1366	4	US-09-289-578-10
9	181	45.9	489	2	US-08-794-795-7
10	181	45.9	489	3	US-09-249-200-7
11	181	45.9	518	1	US-08-392-367B-2
12	181	45.9	518	3	US-08-893-467A-2
13	178.5	45.3	492	4	US-08-468-996-11
14	176	44.7	399	4	US-09-134-000C-6019
15	174.5	44.3	128	4	US-09-227-357-190
16	171	43.4	495	2	US-08-794-795-2
17	171	43.4	495	3	US-09-249-200-2
18	171	43.4	520	2	US-08-794-795-6
19	171	43.4	520	3	US-09-249-200-6
20	170.5	43.3	1017	4	US-08-468-996-10
21	170.5	43.3	1060	3	US-08-931-820-3
22	170.5	43.3	1418	3	US-08-963-825-20
23	170.5	43.3	1418	3	US-09-010-999-1
24	170.5	43.3	1418	4	US-09-500-811-20
25	170.5	43.3	1418	4	US-09-570-573-20
26	170.5	43.3	1418	4	US-09-548-608-20
27	170	43.1	186	4	US-09-366-009-6

28	170	43.1	186	4	US-08-809-156B-6
29	170	43.1	464	2	US-08-836-854-19
30	170	43.1	464	4	US-09-366-009-7
31	170	43.1	464	4	US-08-809-156B-7
32	170	43.1	489	4	US-09-366-009-8
33	170	43.1	489	4	US-08-809-156B-8
34	169.5	43.0	532	1	US-08-494-168-9
35	169.5	43.0	595	3	US-09-219-849-48
36	169.5	43.0	595	3	US-09-219-849-50
37	169.5	43.0	684	1	US-08-555-669-12
38	169.5	43.0	684	3	US-09-073-663-12
39	169.5	43.0	822	3	US-09-219-849-49
40	169	42.9	546	1	US-08-494-168-10
41	169	42.9	557	3	US-09-320-095-10
42	169	42.9	557	3	US-09-523-487-10
43	168.5	42.8	1057	3	US-08-931-820-1
44	168.5	42.8	1341	3	US-08-963-825-18
45	168.5	42.8	1341	4	US-09-500-811-18

ALIGNMENTS

RESULT 1
US-09-453-702B-265
; Sequence 265, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Burland, Valerie
; Perna, Nicole T.
; Plunkett, Guy
; Welch, Rod
; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,702B
; FILING DATE: 03-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 265:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 519 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-453-702B-265

Query Match 52.0%; Score 205; DB 4; Length 519;
Best Local Similarity 54.3%; Pred. No. 1.4e-16;

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Matches 38; Conservative 11; Mismatches 21; Indels 0; Gaps 0;
QY 1 GPKGDDGKDPGEGGKGVGMGPKGKGELGMDGRGNIGKTGPIGKKGKGLL 60
Db 247 GPOGTGPKGDPGVGPKGETGPGVGPQGPAGPKGBRGDVGAQAGVGPAGPRGKGQGERGPQ 306
QY 61 GIPGKKGAG 70
Db 307 GIPGLKGDGTG 316

RESULT 2
US-08-931-820-2
; Sequence 2, Application US/08931820
; Patent No. 6010863
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Assay for collagen degradation
; NUMBER OF SEQUENCES: 4
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION NUMBER: US/08/931,820
; FILING DATE:
; CLASSIFICATION: 435
; APPLICATION DATA: EP 96202596.1
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1024 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: Collagen type I
US-08-931-820-2
Query Match 46.8%; Score 184.5; DB 3; Length 1024;
Best Local Similarity 42.9%; Pred. No. 8.2e-14;
Matches 39; Conservative 9; Mismatches 22; Indels 21; Gaps 2;
QY 1 GPKGDDGKDPGEGGKGVGMGPKGKGELGMDGRGNIGKTGPIGKKGKGLL 51
Db 480 GPSGPAGEVKGKGERGLHGEFGLPGPAGPRGERGPPGESGAAGTGPISGRGSPGPPGD 539
QY 52 GDKGKGLL-----GIPGKKGAG 70
Db 540 GNGKPGVGVGAVGTAGPSGSPGLPGERGAAG 570

RESULT 3
US-08-963-825-19
; Sequence 19, Application US/08963825
; Patent No. 610689
; GENERAL INFORMATION:
; APPLICANT: Qvist, Per
; APPLICANT: Bonde, Martin
; TITLE OF INVENTION: A Method for Assaying Collagen Fragments
; TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
; TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
; TITLE OF INVENTION: Disorders Associated with the Metabolism of
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/963,825
; FILING DATE:
; CLASSIFICATION: 436
; APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US/08/187,319
; FILING DATE: 21-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Cogoris, Adda C
; REGISTRATION NUMBER: 29,714
; REFERENCE/DOCKET NUMBER: 4305/08701
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1366 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: collagen alpha 2- type I
US-08-963-825-19
Query Match 46.8%; Score 184.5; DB 3; Length 1366;
Best Local Similarity 42.9%; Pred. No. 1.1e-13;
Matches 39; Conservative 9; Mismatches 22; Indels 21; Gaps 2;
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Db 559 GPSGPAGEVKGKGERGLHGEFGLPGPAGPRGERGPPGESGAAGTGPISGRGSPGPPGD 618
QY 52 GDKGKGLL-----GIPGKKGAG 70
Db 619 GNGKPGVGVGAVGTAGPSGSPGLPGERGAAG 649

RESULT 4
US-09-500-811-19
; Sequence 19, Application US/09500811
; Patent No. 632314
; GENERAL INFORMATION:
; APPLICANT: Qvist, Per
; APPLICANT: Bonde, Martin
; TITLE OF INVENTION: A Method for Assaying Collagen Fragments
; TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
; TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
; TITLE OF INVENTION: Disorders Associated with the Metabolism of
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: collagen alpha 2- type I
US-09-548-608-19

Query Match      46.8%; Score 184.5; DB 4; Length 1366;
Best Local Similarity 42.9%; Pred. No. 1.1e-13;
Matches 39; Conservative 9; Mismatches 22; Indels 21; Gaps 2;

QY 1 GPKGDDGKGDGEGKHKVGRMGPKIGKLGMDRGNIGKTGPIGKK----- 51
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QY 52 GDKGEKGLL-----GIPGEKKGAG 70
Db 619 GNKGEPGVVGAAGTAGPSGSLPGERGAAG 649

RESULT 7
US-09-585-887-10
; Sequence 10, Application US/09585887
; Patent No. 6413742
; GENERAL INFORMATION:
; APPLICANT: Olsen, David R
; APPLICANT: Chang, Robert
; APPLICANT: McMullin, Hugh
; APPLICANT: Hitzeman, Ronald A.
; APPLICANT: Chisholm, George
; TITLE OF INVENTION: NOVEL METHODS FOR THE PRODUCTION OF GELATIN AND
; TITLE OF INVENTION: FULL-LENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT
; FILE REFERENCE: 225002030400
; CURRENT APPLICATION NUMBER: US/09/585,887
; CURRENT FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/289,578
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/084,828
; PRIOR FILING DATE: 1998-05-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-585-887-10

Query Match      46.8%; Score 184.5; DB 4; Length 1366;
Best Local Similarity 42.9%; Pred. No. 1.1e-13;
Matches 39; Conservative 9; Mismatches 22; Indels 21; Gaps 2;

QY 1 GPKGDDGKGDGEGKHKVGRMGPKIGKLGMDRGNIGKTGPIGKK----- 51
Db 559 GPSGPAGEVKGPKGERGLHGEFGLPGPAGPRGERGPPGESGAAGTGTGIGSRGSPGPPGPD 618
QY 52 GDKGEKGLL-----GIPGEKKGAG 70
Db 619 GNKGEPGVVGAAGTAGPSGSLPGERGAAG 649

RESULT 8
US-09-585-887-10
; Sequence 10, Application US/09289578
; Patent No. 6428978
; GENERAL INFORMATION:
; APPLICANT: Olsen, David R
; APPLICANT: Chang, Robert
; APPLICANT: McMullin, Hugh
; APPLICANT: Hitzeman, Ronald A.
; APPLICANT: Chisholm, George
; TITLE OF INVENTION: NOVEL METHODS FOR THE PRODUCTION OF GELATIN AND
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; TITLE OF INVENTION: FULL-LENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 225002030400
; CURRENT APPLICATION NUMBER: US/09/289,578
; CURRENT FILING DATE: 1999-04-10
; PRIOR APPLICATION NUMBER: 60/084,828
; PRIOR FILING DATE: 1998-05-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-289-578-10

Query Match      46.8%; Score 184.5; DB 4; Length 1366;
Best Local Similarity 42.9%; Pred. No. 1.1e-13;
Matches 39; Conservative 9; Mismatches 22; Indels 21; Gaps 2;

QY 1 GPKGDDGKGDGEGKHKVGRMGPKIGKLGMDRGNIGKTGPIGKK----- 51
Db 559 GPSGPAGEVKGPKGERGLHGEFGLPGPAGPRGERGPPGESGAAGTGTGIGSRGSPGPPGPD 618
QY 52 GDKGEKGLL-----GIPGEKKGAG 70
Db 619 GNKGEPGVVGAAGTAGPSGSLPGERGAAG 649

RESULT 9
US-08-794-795-7
; Sequence 7, Application US/08794795
; Patent No. 5916766
; GENERAL INFORMATION:
; APPLICANT: Elshourlagy, Nabil
; APPLICANT: Adamou, John
; APPLICANT: Gross, Mitchell
; APPLICANT: Lysko, Paul
; TITLE OF INVENTION: Human Macro Scavenger Rec
; TITLE OF INVENTION: eptor
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/794,795
; FILING DATE: 04-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: ATGS0009P
; FILING DATE: 22-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATGS0009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-4026
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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APPLICANT: Tytgvason, Karl
APPLICANT: Elomaa, Outi
APPLICANT: Kangas, Maarit
TITLE OF INVENTION: An Insulated DNA Sequence For a
Patent No. 6063901
TITLE OF INVENTION: No. 6063901el Macrophage Receptor with
TITLE OF INVENTION: A Collagenous Domain and the
TITLE OF INVENTION: Polypeptide Chain Encoded by
TITLE OF INVENTION: such a Sequence
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fay, Sharpe, Beall, Fagan,
ADDRESSEE: Minnich & McKee
STREET: 1100 Superior Avenue
STREET: Suite 700
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2518
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
MEDIUM TYPE: 720 Kb storable
COMPUTER: IBM PS/2, Model 35 SX
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/893,467A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J.
REGISTRATION NUMBER: 24,175
REFERENCE/DOCKET NUMBER: TRV 2 009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 861-5582
TELEFAX: (216) 241-1666
TELEX: (216) 980162
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 518 amino acids
TYPE: amino acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-893-467A-2

Query Match 45.9%; Score 181; DB 3; Length 518;
Best Local Similarity 48.6%; Pred. No. 9.8e-14;
Matches 34; Conservative 10; Mismatches 26; Indels 0; Gaps 0;
QY 1 GPKGDDGKGPGEKGKGVGRMGPKGKIGKGLGMDGRGNIGKTGPIGKKGDKGKGLL 60
DB 192 GPQGPSPKSGEAGLQGLTGAPKQKATGAPGPRGKSGKDGILGTGPKGHEGTKGDKGDL 251
QY 61 GIPGKKGKAG 70
DB 252 GLPGNKGDWG 261
RESULT 13
US-08-468-996-11
Sequence 11, Application US/08468996
Patent No. 6645504
GENERAL INFORMATION:
APPLICANT: Weiner, Howard
APPLICANT: Miller, Ariel
APPLICANT: Zheng, Zheng
APPLICANT: Ahmad, Al-Sabbagh
TITLE OF INVENTION: BYSTANDER SUPPRESSION OF TYPE 1 DIABETES BY ORAL ADMINISTRATION OF
TITLE OF INVENTION: GLUCAGON
FILE REFERENCE: 1010/16959-US3
CURRENT APPLICATION NUMBER: US/08/468,996
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 07/843,752

PRIOR FILING DATE: 1992-02-28
PRIOR APPLICATION NUMBER: US 07/460,852
PRIOR FILING DATE: 1990-02-21
PRIOR APPLICATION NUMBER: US 07/596,936
PRIOR FILING DATE: 1990-10-15
PRIOR APPLICATION NUMBER: US 07/065,734
PRIOR FILING DATE: 1987-06-24
PRIOR APPLICATION NUMBER: US 07/454,486
PRIOR FILING DATE: 1989-12-20
PRIOR APPLICATION NUMBER: US 07/487,732
PRIOR FILING DATE: 1990-03-02
PRIOR APPLICATION NUMBER: US 07/551,632
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: US 07/379,778
PRIOR FILING DATE: 1989-07-14
PRIOR APPLICATION NUMBER: US 07/607,826
PRIOR FILING DATE: 1990-10-31
PRIOR APPLICATION NUMBER: US 07/595,468
PRIOR FILING DATE: 1990-10-10
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patent in version 3.1
SEQ ID NO 11
LENGTH: 492
TYPE: PRT
ORGANISM: Bos taurus
US-08-468-996-11
Query Match 45.3%; Score 178.5; DB 4; Length 492;
Best Local Similarity 50.7%; Pred. No. 1.8e-13;
Matches 37; Conservative 7; Mismatches 26; Indels 3; Gaps 1;
QY 1 GPKGDDGKGPGEKGKGVGRMGPKGKIGKE--LQDMGDRGNIGKTGPIGKKGDKGK 57
DB 406 GPKGANGEPKAGEKGLPGAPGTGPKGAGPAGIAGPKGDRGVDGKGPAGDVGK 465
QY 58 GLLGIPGKKGKAG 70
DB 466 GEVGPSPGPGAKG 478
RESULT 14
US-09-134-000C-6019
Sequence 6019, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patent in version 3.1
SEQ ID NO 6019
LENGTH: 399
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000C-6019
Query Match 44.7%; Score 176; DB 4; Length 399;
Best Local Similarity 49.3%; Pred. No. 2.9e-13;
Matches 33; Conservative 11; Mismatches 23; Indels 0; Gaps 0;
QY 1 GPKGDDGKGPGEKGKGVGRMGPKGKIGKGLGMDGRGNIGKTGPIGKKGDKGKGLL 60
DB 81 GPQGPSPKSGEAGLQGLTGAPKQKATGAPGPRGKSGKDGILGTGPKGHEGTKGDKGDL 140
QY 61 GIPGKKGKAG 67
DB 141 GPQGPSPG 147

RESULT 15
US-09-227-357-190
; Sequence 190, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/227,357
; CURRENT FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,932
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12

; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 190
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (127)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (128)
; OTHER INFORMATION: Xaa equals stop translation
US-09-227-357-190

Query Match 44.3%; Score 174.5; DB 4; Length 128;
Best Local Similarity 52.2%; Pred. No. 1.2e-13;
Matches 35; Conservative 8; Mismatches 21; Indels 3; Gaps 1;

QY 1 GPKDDGEGKDPGEEGKHGKVGKMGPKGKNGELGMDRGNIGKTPIGKKGDKGKGLL 60
DB 62 GRDGRDGRGKGEKGTAGLRGKTGPLGLAGE---KGDQGETGKGPIGPEGEKGEVGP 118
QY 61 GIPGEGK 67
DB 119 GPPGPKG 125

Search completed: March 8, 2004, 12:17:27
Job time : 19.7137 secs

No good data

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OM protein - protein search, using sw model

Run on: March 8, 2004, 11:54:00 ; Search time 66.2907 seconds

(without alignments)
306.882 Million cell updates/sec

Title: US-09-600-932-2_COPY_47_118

Perfect score: 394

Sequence: 1 GPKGDDGKGPGEKGK.....DKGKGLLIPGKGRAGTV 72

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Genesep29Jan04.*
- 2: Genesep1980s.*
- 3: Genesep1990s.*
- 4: Genesep2000s.*
- 5: Genesep2001s.*
- 6: Genesep2002s.*
- 7: Genesep2003as.*
- 8: Genesep2003bs.*
- 9: Genesep2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	394	100.0	277	2	AAY25518 Human col
2	390	99.0	277	2	AAY41698 Human PRO
3	390	99.0	277	3	AAB44254 Human PRO
4	390	99.0	277	4	AAB29073 Human PRO
5	390	99.0	277	6	ABU58449 Human PRO
6	390	99.0	277	6	ABU87997 Novel hum
7	390	99.0	277	6	ABU84312 Human sec
8	390	99.0	277	6	ABR66186 Human sec
9	390	99.0	277	6	ABR65576 Human sec
10	390	99.0	277	6	ABU99516 Human sec
11	390	99.0	277	6	ABU82755 Human PRO
12	390	99.0	277	6	ABU89876 Novel hum
13	390	99.0	277	6	ABR68125 Human sec
14	390	99.0	277	6	ABU96178 Novel hum
15	390	99.0	277	6	ABU92609 Human sec
16	390	99.0	277	6	ABO08686 Human sec
17	390	99.0	277	6	ABO02738 Human sec
18	390	99.0	277	6	ABR74892 Human sec
19	390	99.0	277	6	ABR94654 Human sec
20	390	99.0	277	6	ABO25200 Novel hum
21	390	99.0	277	6	ABU85627 Human PRO
22	390	99.0	277	6	ABU98787 Novel hum
23	390	99.0	277	6	ABU98002 Novel hum
24	390	99.0	277	6	ABU91708 Novel hum
25	390	99.0	277	6	ABU72206 Novel hum

26	390	99.0	277	6	ABU89401 Human PRO
27	390	99.0	277	6	ABU86242 Human sec
28	390	99.0	277	6	ABU67455 Human sec
29	390	99.0	277	6	ABU80483 Human PRO
30	390	99.0	277	6	ABR99401 Human sec
31	390	99.0	277	6	ABR98791 Human sec
32	390	99.0	277	6	ABO16314 Human sec
33	390	99.0	277	6	ABR92214 Human sec
34	390	99.0	277	6	ABO18855 Human sec
35	390	99.0	277	6	ABR78276 Human sec
36	390	99.0	277	6	ABU85012 Novel hum
37	390	99.0	277	6	ABO00151 Human sec
38	390	99.0	277	6	ABO11483 Human sec
39	390	99.0	277	6	ABO02128 Human sec
40	390	99.0	277	6	ABU88702 Human sec
41	390	99.0	277	6	ABU83397 Human sec
42	390	99.0	277	6	ABO06198 Novel hum
43	390	99.0	277	6	ABR59234 Human sec
44	390	99.0	277	6	ABO09296 Human sec
45	390	99.0	277	6	ABO19160 Novel hum

ALIGNMENTS

RESULT 1

AAY25518
ID AAY25518 standard; protein; 277 AA.

XX AC AAY25518;
XX DT 30-SEP-1999 (first entry)
XX DE Human collectin protein.
XX KW Collectin; human; antibacterial; antiviral; treatment; infection.
XX OS Homo sapiens.
XX FN WO9937767-A1.
XX DT 29-JUL-1999.
XX PF 24-JUL-1998; 98WO-JP003328.
XX PR 23-JAN-1998; 98JP-00011281.
XX PA (FUSO) FUSO PHARM IND LTD.
XX PI Wakamiya N;
XX DR WPI; 1999-458691/38.
XX DR N-PSDB; AAX88323.
XX PT New collectin protein of human origin and DNA encoding it.
XX PS Claim 1; Page 42-44; 58pp; Japanese.
XX CC This invention describes the isolation and characterisation of a novel human collectin protein and its encoding polynucleotide. The human collectin exhibits antibacterial and antiviral activity and can be used as an agent for the treatment of human bacterial and viral infections.
XX CC This sequence represents the novel human collectin
SQ Sequence 277 AA;

Query Match 100.0%; Score 394; DB 2; Length 277;
Best Local Similarity 100.0%; Pred. No. 8e-37;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGDDGKGPGEKGKVGKVGKGLLMDRGNIGTKTGPICKGKGLL 60
|||||
DB 47 GPKGDDGKGPGEKGKVGKVGKGLLMDRGNIGTKTGPICKGKGLL 106

QY	61	GIPGEKKGAGTV 72	PR	27-APR-1998;	98US-00833336P.
Db	107	GIPGEKKGAGTV 118	PR	28-APR-1998;	98US-00833332P.
			PR	29-APR-1998;	98US-00833392P.
			PR	29-APR-1998;	98US-00834355P.
			PR	29-APR-1998;	98US-00834366P.
			PR	29-APR-1998;	98US-00834399P.
			PR	29-APR-1998;	98US-00835000P.
			PR	29-APR-1998;	98US-00835454P.
			PR	29-APR-1998;	98US-00835558P.
			PR	29-APR-1998;	98US-00835599P.
			PR	30-APR-1998;	98US-00837422P.
			PR	05-MAY-1998;	98US-00843666P.
			PR	06-MAY-1998;	98US-00844144P.
			PR	06-MAY-1998;	98US-00844411P.
			PR	07-MAY-1998;	98US-00845988P.
			PR	07-MAY-1998;	98US-00846000P.
			PR	07-MAY-1998;	98US-00846377P.
			PR	07-MAY-1998;	98US-00846377P.
			PR	07-MAY-1998;	98US-00846399P.
			PR	07-MAY-1998;	98US-00846400P.
			PR	07-MAY-1998;	98US-00846433P.
			PR	13-MAY-1998;	98US-00853232P.
			PR	13-MAY-1998;	98US-00853338P.
			PR	13-MAY-1998;	98US-00853399P.
			PR	15-MAY-1998;	98US-00855737P.
			PR	15-MAY-1998;	98US-00855799P.
			PR	15-MAY-1998;	98US-00855800P.
			PR	15-MAY-1998;	98US-00855822P.
			PR	15-MAY-1998;	98US-00855822P.
			PR	15-MAY-1998;	98US-00856899P.
			PR	15-MAY-1998;	98US-00856977P.
			PR	15-MAY-1998;	98US-00857000P.
			PR	15-MAY-1998;	98US-00857044P.
			PR	18-MAY-1998;	98US-00860233P.
			PR	22-MAY-1998;	98US-00863322P.
			PR	22-MAY-1998;	98US-00864414P.
			PR	22-MAY-1998;	98US-00864430P.
			PR	22-MAY-1998;	98US-00864866P.
			PR	28-MAY-1998;	98US-00870988P.
			PR	28-MAY-1998;	98US-00871066P.
			PR	28-MAY-1998;	98US-00872088P.
			PR	30-JUL-1998;	98US-00946511P.
			PR	11-SEP-1998;	98US-01000388P.
			XX	(GETH) GENENTECH INC.	
			PA	Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;	
			PI	WPI: 1999-551358/46.	
			DR	N-PSDB; AA333973.	
			XX	New secreted and transmembrane polypeptides and their polynucleotides,	
			PT	useful for treating blood coagulation disorders, cancers and cellular	
			PT	adhesion disorders.	
			XX	Claim 12; Fig 37; 530pp; English.	
			PS	The present invention describes secreted and transmembrane polypeptides	
			XX	and their polynucleotides. The nucleotide sequences are useful as sources	
			CC	of probes, primers, for chromosome mapping, and for generation of	
			CC	antisense sequences. They can also be used to create transgenic animals.	
			CC	The proteins can be used to treat a variety of diseases and disorders,	
			CC	depending on their function. Diseases that may be treated include blood	
			CC	coagulation disorders, cancers and cellular adhesion disorders. They may	
			CC	also be used to raise antibodies. AA333891 to AA334338, and AA41685 to	
			CC	AA41774 represent polynucleotide and polypeptide sequence given in the	
			CC	exemplification of the present invention	
			XX	Sequence 277 AA;	
			SQ	Query Match 99.0%; Score 390; DB 2; Length 277;	
				Best Local Similarity 98.6%; Pred. No. 2.3e-36;	
				Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	

RESULT 2
AA41698
ID AA41698 standard; protein; 277 AA.

AC AA41698;
XX
DT 07-DEC-1999 (first entry)
XX
DE Human PRO702 protein sequence.
XX
KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein.

OS Homo sapiens.

XX

PN WO9946281-A2.

XX

PD 16-SEP-1999.

XX

PF 08-MAR-1999;

XX

PR 10-MAR-1998;

PR

PR 11-MAR-1998;

PR

PR 11-MAR-1998;

PR

PR 11-MAR-1998;

PR

PR 11-MAR-1998;

PR

PR 11-MAR-1998;

PR

PR 11-MAR-1998;

PR

PR 11-MAR-1998;

PR

PR 11-MAR-1998;

PR

PR 11-MAR-1998;

PR

PR 11-MAR-1998;

PR

PR 11-MAR-1998;

PR

PR 11-MAR-1998;

PR

QY 1 GPKGDDGKGDGCEGKHGKVGKGMGPKGKGELGDMGDRGNIGKTGPIGKKGDKGKGLL 60
Db 47 GPKGDDGKGDGCEGKHGKVGKGMGPKGKGELGDMGDRGNIGKTGPIGKKGDKGKGLL 106
QY 61 GIPGKKGKAGTV 72
Db 107 GIPGKKGKAGTV 118

RESULT 3
AAB44254
ID AAB44254 standard; protein; 277 AA.
XX AAB44254;
XX 08-FEB-2001 (first entry)
XX Human PRO702 (UNQ366) protein sequence SEQ ID NO:97.
DE Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
KW expressed sequence tag; detection; cancer.
XX Homo sapiens.
OS
XX WO200053756-A2.
XX 14-SEP-2000.
XX 18-FEB-2000; 2000WO-US004341.
XX 08-MAR-1999; 99WO-US005028.
XX 13-MAR-1999; 99US-0123957P.
XX 23-MAR-1999; 99US-0126773P.
XX 21-APR-1999; 99US-0130232P.
XX 28-APR-1999; 99US-0133445P.
XX 14-MAY-1999; 99US-0134287P.
XX 23-JUN-1999; 99US-0141037P.
XX 26-JUL-1999; 99US-0145698P.
XX 29-OCT-1999; 99US-0162506P.
XX 30-NOV-1999; 99WO-US028313.
XX 02-DEC-1999; 99WO-US028551.
XX 02-DEC-1999; 99WO-US028565.
XX 16-DEC-1999; 99WO-US030095.
XX 30-DEC-1999; 99WO-US031243.
XX 30-DEC-1999; 99WO-US031274.
XX 05-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000272.
XX 06-JAN-2000; 2000WO-US000376.
PA (GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen MB;
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Kljavin LJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WJ;
XX WPI; 2000-611443/58.
DR N-PSDB; AAC78480.
XX Novel PRO polypeptides and polynucleotides used in detection methods, to
PT target bioactive molecules to specific cells, and to modulate cellular
PT activities.
XX Claim 12; Fig 37; 636pp; English.
XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
CC tag) sequences which encode secreted or transmembrane PRO polypeptides.
CC The PRO polynucleotides and polypeptides have cytostatic activity. The
CC polynucleotides and polypeptides can be used for detecting the presence
CC of PRO polypeptides in samples, for linking bioactive molecules to cells
CC and for modulating biological activities of cells, using the polypeptides

CC for specific targeting. The polypeptide targeting can be used to kill the
CC target cells, e.g. for the treatment of cancers. The polypeptide pairs
CC provide specific targeting of bioactive molecules to cells. AAC78600 to
CC AAC78987 represent PCR primers and probes used in the isolation of the
CC PRO polynucleotide sequences
XX
SQ Sequence 277 AA;

Query Match 99.0%; Score 390; DB 3; Length 277;
Best Local Similarity 98.6%; Pred. No. 2.3e-36;
Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPKGDDGKGDGCEGKHGKVGKGMGPKGKGELGDMGDRGNIGKTGPIGKKGDKGKGLL 60
Db 47 GPKGDDGKGDGCEGKHGKVGKGMGPKGKGELGDMGDRGNIGKTGPIGKKGDKGKGLL 106
QY 61 GIPGKKGKAGTV 72
Db 107 GIPGKKGKAGTV 118

RESULT 4
AAU29073
ID AAU29073 standard; protein; 277 AA.
XX AAU29073;
AC AAU29073;
XX 18-DEC-2001 (first entry)
DT Human PRO polypeptide sequence #50.
DE
XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX Homo sapiens.
XX WO200168848-A2.
XX 20-SEP-2001.
XX 28-FEB-2001; 2001WO-US006520.
XX 01-MAR-2000; 2000WO-US005601.
XX 02-MAR-2000; 2000WO-US005841.
XX 03-MAR-2000; 2000US-0187202P.
XX 06-MAR-2000; 2000US-0186968P.
XX 14-MAR-2000; 2000US-0189320P.
XX 14-MAR-2000; 2000US-0189328P.
XX 15-MAR-2000; 2000WO-US006884.
XX 21-MAR-2000; 2000US-0190828P.
XX 21-MAR-2000; 2000US-0191007P.
XX 21-MAR-2000; 2000US-0191048P.
XX 21-MAR-2000; 2000US-0191314P.
XX 28-MAR-2000; 2000US-0192655P.
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XX 17-MAY-2000; 2000WO-US013705.

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PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
XX (GETH) GENENTECH INC.
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2001-602746/68.
DR N-PSDB; AAS45974.
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.
XX Claim 11; Fig 100; 774pp; English.
XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumour in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders
XX Sequence 277 AA;
SQ
Query Match 99.0%; Score 350; DB 4; Length 277;
Best Local Similarity 98.6%; Pred. No. 2.3e-36;
Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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DB 47 GPKGDDGKDPGEGKCKKVCGRMGPKCKGELGDMGDRGNIGKTGTGKKGKGLL 106
QY 61 GIPGEXGKAGTV 72
DB 107 GIPGEXGKAGTV 118
RESULT 5
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XX AC ABUS8449;
XX DT 15-APR-2003 (first entry)
XX Human PRO polypeptide #50.
XX Human; PRO; cystostatic; tumour; cancer; breast; lung; stomach; liver;
KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX OS Homo sapiens.
XX

PN US2003027272-A1.
XX 06-FEB-2003.
XX 21-JUN-2002; 2002US-00176492.
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XX	ABU87997;
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DT	07-JUL-2003 (first entry)
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XX	Human; secreted and transmembrane protein: PRO; gene therapy;
XX	tumour necrosis factor-alpha release; TNF-alpha release;
KW	chondrocyte proliferation; chondrocyte differentiation; tumour;
KW	adrenal tumour; lung tumour; colon tumour; breast tumour;
KW	prostate tumour; rectal tumour; cervical tumour; liver tumour.
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CS	Homo sapiens.
XX	
PN	US2003032127-A1.
PN	

XX 13-FEB-2003.
PD 26-JUN-2002; 2002US-00183012.
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XX KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;

XX KW tissue typing.

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RESULT 11
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XX DT 27-JUN-2003 (first entry)
XX DE Human PRO polypeptide #50.
XX KW Human; PRO polypeptide; secreted and transmembrane protein; tumour;
XX KW chromosome mapping; gene mapping; cytostatic.
XX OS Homo sapiens.
XX PN US2003032113-A1.
XX PD 13-FEB-2003.
XX PF 20-JUN-2002; 2002US-00176911.
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Best Local Similarity 98.6%; Pred. No. 2.3e-36;

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ID ABU89876 standard; protein; 277 AA.

XX AC ABU89876;

XX DT 11-AUG-2003 (first entry)

XX DE Novel human secreted and transmembrane protein PRO702.
XX KW Human; gene therapy; tissue typing; tumour; chondrocyte proliferation;
XX KW chondrocyte differentiation; tumour necrosis factor-alpha release;
XX KW affinity purification.

XX OS Homo sapiens.

XX PN US2003036147-A1.

XX PD 20-FEB-2003.

XX PF 02-JUL-2002; 2002US-00187741.

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Best Local Similarity 98.6%; Pred. No. 2.3e-36;
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Db 107 GIPGEKKGAGTV 118

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AC ABR68125;
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DT 11-AUG-2003 (first entry)
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DE Human secreted polypeptide PRO702, SEQ ID NO:100.
XX
KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnery; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003027264-A1.
XX
PD 06-FEB-2003.
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PF 18-JUN-2002; 2002US-00174579.
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Best Local Similarity 98.6%; Pred. No. 2.3e-36; Mismatches 1; Indels 0; Gaps 0;
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QY 61 GIPGKKGAGTV 72

Db 107 GIPGKKGAGTV 118

RESULT 14

ABU96178
ID ABU96178 standard; protein; 277 AA.

XX AC ABU96178;

XX DT 25-JUL-2003 (first entry)

XX DE Novel human secreted and transmembrane protein PRO702.

XX KW Human; secreted and transmembrane protein; PRO; transgenic animal;
XX KW knockout; chromosome identification; tissue typing; tumour;
XX KW chondrocyte proliferation; chondrocyte differentiation;
XX KW tumor necrosis factor-alpha release stimulator.

XX OS Homo sapiens.

XX PN US2003036144-A1.

XX PD 20-FEB-2003.

XX PF 01-JUL-2002; 2002US-00187601.

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Query Match 99.0%; Score 390; DB 6; Length 277;
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Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GIPGEGKAGTV 72
Db 107 GIFGEGKAGTV 118

RESULT 15
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XX AC ABU92609;
XX DT 18-JUL-2003 (first entry)
XX DE Human secreted/transmembrane protein (PRO) #50.
XX KW Human; secreted protein; transmembrane protein; PRO; tumour;
XX KW proliferation; differentiation; chondrocyte cell; TNF-alpha;
XX KW tumour necrosis factor-alpha; gene therapy.
XX OS Homo sapiens.
XX PN US2003036149-A1.
XX PD 20-FEB-2003.
XX PF 02-JUL-2002; 2002US-00187746.
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Query Match 99.0%; Score 390; DB 6; Length 277;
Best Local Similarity 98.6%; Pred. No. 2.3e-36;
Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPKGDDGKGDPPGEGKHGKVGKMGPKGKGELGDMGDRGNIGKTGPIGKKGDKGKGLL 60
DB 47 GPKGDDGKGDPPGEGKHGKVGKMGPKGKGELGDMGDRGNIGKTGPIGKKGDKGKGLL 106
QY 61 GIPGKKGKAGTV 72
DB 107 GIPGKKGKAGTV 118

Search completed: March 8, 2004, 12:11:22
Job time : 66.2907 secs

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OM protein - protein search, using sw model

Run on: March 8, 2004, 11:56:05 ; Search time 4.5912 Seconds

(without alignments)
328.331 Million cell updates/sec

Title: US-09-600-932-2_COPY_119_147

Perfect score: 153

Sequence: 1 CDCGRYKFKVQLDISARLTKSMKFKVN 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	34.0	3718	1 LMA5 MOUSE	Q61001 mus musculus
2	51	33.3	4473	1 PLE1 CRGR	Q91155 cricetus
3	49	32.0	492	1 PLE1 BOVIN	P00743 bos taurus
4	49	32.0	964	1 PLE1 MOUSE	Q9QX81 mus musculus
5	49	32.0	1239	1 TOP2 CRIFA	F27570 crithidia f
6	49	32.0	4684	1 PLE1 HUMAN	Q15149 homo sapien
7	49	32.0	4687	1 PLE1 RAT	P30427 rattus norv
8	47	30.7	265	1 FPHD STAM	Q9YX22 staphylococ
9	47	30.7	265	1 FPHD STAM	Q8N955 staphylococ
10	47	30.7	283	1 CBP3 SCHPO	Q9U866 schizosacch
11	47	30.7	287	1 PANC COREF	Q8F8A6 corynebacte
12	46.5	30.4	490	1 FA10 RABIT	Q19345 oryctolagus
13	46	30.1	279	1 PANC CORGL	Q9X713 corynebacte
14	46	30.1	519	1 LEU1 CANBF	Q7V416 candidatus
15	46	30.1	604	1 YJ16 YEAST	P47112 saccharomyc
16	46	30.1	1035	1 DPOL RHOM6	O71121 rhesus cyto
17	45.5	29.7	167	1 MCRW METJA	Q57582 methanococc
18	45.5	29.7	1236	1 TOP2 LEICH	Q61078 leishmania
19	45	29.4	403	1 ARGJ CAUCR	Q9A3Y4 c arginine
20	45	29.4	488	1 FA10 HUMAN	P00742 homo sapien
21	45	29.4	496	1 DFN5 HUMAN	Q60443 homo sapien
22	45	29.4	540	1 AXR1 ARATH	P42744 arabidopsis
23	45	29.4	643	1 VP40 HSV2	P52369 equine herp
24	45	29.4	689	1 TGM2 CAVCU	P08587 cavia cutie
25	45	29.4	1232	1 RSP2 TRYCR	P30190 trypanosoma
26	44.5	29.1	52	1 T014 HALNI	Q8HPC0 halobacteri
27	44.5	29.1	164	1 Y0HA SALTI	Q823Q8 salmonella
28	44.5	29.1	164	1 Y0HA SALTI	Q8ZML3 salmonella
29	44	28.8	126	1 URE2 BACPA	P41021 bacillus pa
30	44	28.8	363	1 MRAY STRCO	P56833 streptomyce
31	44	28.8	571	1 UREL STAPB	Q8CNC9 staphylococ
32	44	28.8	975	1 KINH DROME	P17210 drosophila
33	44	28.8	1180	1 ITAL RAT	P18514 rattus norv

ALIGNMENTS

RESULT 1

ID	LMA5 MOUSE	STANDARD;	PRT;	3718 AA.
AC	Q61001; 09JHO6;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Laminin alpha-5 chain precursor.			
GN	LMA5.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
[1]				
RP	SEQUENCE OF 1-92 FROM N.A., AND SEQUENCE OF 41-46.			
RA	MEDLINE=21818471; PubMed=11829758;			
RA	Garbe J.H., Gohring W., Mann K., Timpl R., Sasaki T.;			
RT	"Complete sequence, recombinant analysis and binding to laminins and sulphated ligands of the N-terminal domains of laminin alpha3B and alpha5 chains.";			
RT	Biochem. J. 362:113-221 (2002).			
[2]				
RP	SEQUENCE OF 84-3718 FROM N.A.			
RC	STRAIN=C57BL/6 X CBA; TISSUE=Lung;			
RA	MEDLINE=96081906; PubMed=7499364;			
RA	Miner J.H., Lewis R.M., Sanes J.R.;			
RT	"Molecular cloning of a novel laminin chain, alpha 5, and widespread expression in adult mouse tissues.";			
RL	J. Biol. Chem. 270:28523-28526 (1995).			
[3]				
RP	REVISIONS.			
RA	Miner J.H., Lewis R.M., Sanes J.R.;			
RL	Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: Binding to cells via a high affinity receptor, laminin is thought to mediate the attachment, migration and organization of cells into tissues during embryonic development by interacting with other extracellular matrix components.			
CC	-!- FUNCTION: ALPHA-5 CHAIN MAY BE THE MAJOR LAMININ ALPHA CHAIN OF ADULT EPITHELIAL AND/OR ENDOTHELIAL BASAL LAMINAE.			
CC	-!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three different polypeptide chains (alpha, beta, gamma), which are bound to each other by disulfide bonds into a cross-shaped molecule comprising one long and three short arms with globules at each end.			
CC	-!- SUBCELLULAR LOCATION: Extracellular; found in the basement membranes (major component).			
CC	-!- TISSUE SPECIFICITY: In adult, high levels in heart, lung, and kidney; lower in brain, muscle and testis; very low in liver, gut and skin.			
CC	-!- DOMAIN: The alpha-helical domains I and II are thought to interact with other laminin chains to form a coiled coil structure.			
CC	-!- DOMAIN: Domains VI, IV and G are globular.			
CC	-!- SIMILARITY: Contains 1 laminin N-terminal domain.			
CC	-!- SIMILARITY: Contains 22 laminin EGF-like domains.			
CC	-!- SIMILARITY: Contains 2 laminin IV domains.			
CC	-!- SIMILARITY: Contains 5 laminin G-like domains.			

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CC -----
CC EMBL; A0293593; CAB99255.1; --
CC EMBL; U37501; AAC53430.1; --
CC PIR; T10053; T10053.
CC HSSP; P02468; 1TLE.
CC MGD; MGI:105382; Lama5.
CC GO; GO:0005604; C:basement membrane; IDA.
CC GO; GO:0008178; P:integrin binding; IDA.
CC GO; GO:003024; P:lung development; IMP.
CC InterPro; IPR008985; CoR_A-like lec_gl.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR008212; Lam N2.
CC InterPro; IPR000034; Laminin B.
CC InterPro; IPR002049; Laminin_EGF.
CC InterPro; IPR001791; Laminin_G.
CC InterPro; IPR008211; LamN1.
CC Pfam; PF00052; laminin_B; 1.
CC Pfam; PF00053; laminin_EGF; 17.
CC Pfam; PF00054; laminin_G; 2.
CC Pfam; PF00055; laminin_Nterm; 1.
CC PRINTS; PR00011; EGF_LAMININ.
CC ProDom; PD002082; Lam N2; 1.
CC ProDom; PD003031; Laminin_B; 1.
CC SMART; SM00180; EGF_Lam; 20.
CC SMART; SM00281; LamB; 1.
CC SMART; SM00282; LamG; 5.
CC SMART; SM00136; LamN1; 1.
CC PROSITE; PS00022; EGF_1; 19.
CC PROSITE; PS01186; EGF_2; 3.
CC PROSITE; PS01248; LAMININ TYPE_EGF; 19.
CC PROSITE; PS00025; LAM_G_DOMAIN; 5.
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
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FT DOMAIN 41 3718 LAMININ ALPHA-5 CHAIN.
FT DOMAIN 41 304 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 305 363 LAMININ EGF-LIKE 1.
FT DOMAIN 364 433 LAMININ EGF-LIKE 2.
FT DOMAIN 434 479 LAMININ EGF-LIKE 3.
FT DOMAIN 500 546 LAMININ EGF-LIKE 4.
FT DOMAIN 547 592 LAMININ EGF-LIKE 5.
FT DOMAIN 593 637 LAMININ EGF-LIKE 6.
FT DOMAIN 638 682 LAMININ EGF-LIKE 7.
FT DOMAIN 683 728 LAMININ EGF-LIKE 8.
FT DOMAIN 729 781 LAMININ EGF-LIKE 9.
FT DOMAIN 782 833 LAMININ EGF-LIKE 10.
FT DOMAIN 834 855 LAMININ EGF-LIKE 11 (INCOMPLETE).
FT DOMAIN 856 1442 LAMININ EGF-LIKE 11 (DOMAIN IV B).
FT DOMAIN 1443 1488 LAMININ EGF-LIKE 12.
FT DOMAIN 1489 1532 LAMININ EGF-LIKE 13.
FT DOMAIN 1533 1581 LAMININ EGF-LIKE 14.
FT DOMAIN 1582 1632 LAMININ EGF-LIKE 15.
FT DOMAIN 1633 1642 LAMININ EGF-LIKE 16 (N-TERMINAL).
FT DOMAIN 1643 1831 LAMININ EGF-LIKE 16 (DOMAIN IV A).
FT DOMAIN 1832 1864 LAMININ EGF-LIKE 16 (C-TERMINAL).
FT DOMAIN 1865 1914 LAMININ EGF-LIKE 17.
FT DOMAIN 1915 1970 LAMININ EGF-LIKE 18.
FT DOMAIN 1971 2024 LAMININ EGF-LIKE 19.
FT DOMAIN 2025 2071 LAMININ EGF-LIKE 20.
FT DOMAIN 2072 2118 LAMININ EGF-LIKE 21.
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DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN F10.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoides;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN (1)_SEQUENCE OF 1-487 FROM N.A.
RP MEDLINE=84247315; PubMed=6330671;
RA Fung M.R., Campbell R.M., McGillivray R.T.A.;
RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
RT containing a prepro leader sequence."
RL Nucleic Acids Res. 12:4481-4492(1984).
RN (2)
RP SEQUENCE OF 41-180.
RX MEDLINE=80130563; PubMed=6766735;
RA Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
RA Titani K.;
RT "Amino acid sequence of the light chain of bovine factor X1 (Stuart
RT factor).";
RL Biochemistry 19:659-667(1980).
RN (3)
RP REVISION TO 103.
RX MEDLINE=83308813; PubMed=6688526;
RA McMullen B.A., Fujikawa K., Kisiel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
RT K-dependent blood coagulation zymogens."
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN (4)
RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX MEDLINE=76053069; PubMed=1059093;
RA Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
RA Neurath H.;
RT "Bovine factor X1 (Stuart factor): amino-acid sequence of heavy
RT chain."
RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
RN (5)
RP SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=94062825; PubMed=8243461;
RA Inoue K., Morita T.;
RT "Identification of O-linked oligosaccharide chains in the activation
RT peptides of blood coagulation factor X. The role of the carbohydrate
RT moieties in the activation of factor X."
RL Eur. J. Biochem. 218:153-163(1993).
RN (6)
RP ACTIVE SITE.
RX MEDLINE=73053314; PubMed=4264286;
RA Titani K., Hermodson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
RA Neurath H., Davie E.W.;
RT "Bovine factor X1a (activated Stuart factor). Evidence of homology
RT with mammalian serine proteases."
RL Biochemistry 11:4899-4903(1972).
RN (7)
RP PROCESSING.
RX MEDLINE=76053121; PubMed=1059122;
RA Fujikawa K., Titani K., Davie E.W.;
RT "Activation of bovine factor X (Stuart factor): conversion of factor
RT Xa-alpha to factor Xa-beta."
RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
RN (8)
RP CALCIUM-BINDING DATA.
RX MEDLINE=84185716; PubMed=6546930;
RA Sugo T., Bjoerk I., Holmgren A., Stenflo J.;
RT "Calcium-binding properties of bovine factor X lacking the gamma-
RT carboxyglutamic acid-containing region."
RL J. Biol. Chem. 259:5705-5710(1984).
RN (9)
RP SULFATION.
RX MEDLINE=86140210; PubMed=3949800;
RA Morita T., Jackson C.M.;
RT "Localization of the structural difference between bovine blood
RT coagulation factors X1 and X2 to tyrosine 18 in the activation

peptide".
J. Biol. Chem. 261:4008-4014(1986).
RN (10)
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=91084483; PubMed=2261466;
RA Selander M., Persson E., Stenflo J., Drakenberg T.;
RT "1H NMR assignment and secondary structure of the Ca2(+)-free form of
RT the amino-terminal epidermal growth factor like domain in coagulation
RT factor X";
RL Biochemistry 29:8111-8118(1990).
RN (11)
RP STRUCTURE BY NMR OF 85-136.
RX MEDLINE=92329412; PubMed=1627540;
RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
RA Telemann O.;
RT "Three-dimensional structure of the apo form of the N-terminal
RT EGF-like module of blood coagulation factor X as determined by NMR
RT spectroscopy and simulated folding."
RL Biochemistry 31:5974-5983(1992).
RN (12)
RP STRUCTURE BY NMR OF 85-136.
RX MEDLINE=92406922; PubMed=1527084;
RA Selander-Sunnerhagen M., Ullner M., Persson E., Telemann O.,
RA Stenflo J., Drakenberg T.;
RT "How an epidermal growth factor (EGF)-like domain binds calcium. High
RT resolution NMR structure of the calcium form of the NH2-terminal EGF-
RT like domain in coagulation factor X."
RL J. Biol. Chem. 267:19642-19649(1992).
RN (13)
RP STRUCTURE BY NMR OF 41-136.
RX MEDLINE=96387194; PubMed=8794734;
RA Sunnerhagen M., Olah G.A., Stenflo J., Forsen S., Drakenberg T.,
RA Trewnella J.;
RT "The relative orientation of Gla and EGF domains in coagulation
RT factor X is altered by Ca2+ binding to the first EGF domain. A
RT combined NMR-small angle X-ray scattering study."
RL Biochemistry 35:11547-11559(1996).
RN (14)
RP FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
RP converts prothrombin to thrombin in the presence of factor Va,
RP calcium and phospholipid during blood clotting.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
CC Arg-|-Ile bonds in prothrombin to form thrombin.
CC -!- SUBUNIT: The two chains are formed from a single-chain precursor
CC by the excision of two Arg residues and are held together by 1 or
CC more disulfide bonds.
CC -!- PTM: The vitamin K-dependent, enzymatic carboxylation of some
CC glutamate residues allows the modified protein to bind calcium.
CC -!- PTM: N- and O-glycosylated.
CC -!- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
CC -!- MISCELLANEOUS: Calcium also binds, with stronger affinity to
CC another site, beyond the GLA domain.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch.
CC -----
CC EMBL; X00673; CAA25286.1; -.
CC PIR; A22867; EXBO.
CC PDB; 1AJO; 31-JAN-94.
CC PDB; 1CCF; 31-MAY-94.
CC PDB; 1WHE; 15-MAY-97.
CC PDB; 1WHP; 15-MAY-97.
CC PDB; 1IOD; 21-JAN-03.
CC PDB; 1KIG; 28-OCT-98.
CC MEROPS; S01.216; -.
CC GlycoSuiteDB; P00743; -.

DR InterPro: IPR000152; Asx hydroxyl S.
DR InterPro: IPR009003; Cys_ser_trypsin.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ga.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR002383; GLA blood.
DR InterPro: IPR001254; Peptidase S1.
DR InterPro: IPR001314; Peptidase S1A.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF; 2.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; TRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; Tryp_Spc; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00026; EGF_3; 1.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
KW Signal; Zymogen; EGF-like domain; Repeat; Sulfation; 3D-structure.
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FT PROPEP 24 40
FT CHAIN 41 180
FT CHAIN 181 492
FT PROPEP 183 233
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FT PROPEP 476 492
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Query Match 32.0%; Score 49; DB 1; Length 492;
Best Local Similarity 40.0%; Pred. No. 6.1;
Matches 10; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
QY 5 RYRKFGVGLDLSIARKLTKSMKFKVN 29
DB 312 RFVKETYDFDIAVLRLTKTFIRFN 336
RESULT 4
ID PLE1_MOUSE
AC Q9QXS1; Q9CS65; Q9QUT2; Q9QXQ8; Q9QXQ9; Q9QXR0; Q9QXR1; Q9QXR2;
AC Q9QXR3; Q9QXR4; Q9QXR5; Q9QXR6; Q9QXR7; Q9QXR8; Q9QXR9; Q9QXS0;
AC Q9QXS2; Q9QXS3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Plectin 1 (PLTN) (PCN) (fragment).
GN PLEC1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
RC TISSUE=Brain, Embryo, Heart, Kidney, Skeletal muscle, and Testis;
RX MEDLINE=20025755; PubMed=1056294;
RA Fuchs P., Zoerer M., Reznicek G.A., Spazierer D., Oehler S.,
RA Castanon M.J., Hauptmann R., Wiche G.;
RT "Unusual 5' transcript complexity of plectin isoforms: novel tissue-
specific exons modulate actin binding activity.";
RL Hum. Mol. Genet. 8:2461-2472(1999).
RN [2]
RP SEQUENCE OF 181-812 FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojochori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gusticich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- FUNCTION: Interlinks intermediate filaments with microtubules and
microfilaments and anchors intermediate filaments to desmosomes or
hemidesmosomes. May be involved not only in the crosslinking and
stabilization of cytoskeletal intermediate filaments network, but
also in the regulation of their dynamics.
CC -!- SUBUNIT: Homodimer or homotetramer (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=16;
CC Name=PLEC-1.2A;
CC IsoId=Q9QXS1-1; Sequence=VSP_005048;
CC Name=PLEC-1;
CC IsoId=Q9QXS1-2; Sequence=VSP_005048;
CC Name=PLEC-1A;
CC IsoId=Q9QXS1-3; Sequence=VSP_005036, VSP_005045, VSP_005048;
CC Name=PLEC-1B.2A;
CC IsoId=Q9QXS1-4; Sequence=VSP_005037, VSP_005045;
CC Name=PLEC-1B;
CC IsoId=Q9QXS1-5; Sequence=VSP_005037, VSP_005045, VSP_005048,
VSP_005048;
CC Name=PLEC-0.1C;
CC IsoId=Q9QXS1-6; Sequence=VSP_005039, VSP_005047, VSP_005048;
CC Name=PLEC-0.1C.2A;
CC IsoId=Q9QXS1-7; Sequence=VSP_005039;
CC Name=PLEC-0.1C.2A.3A;
CC IsoId=Q9QXS1-8; Sequence=VSP_005039, VSP_005047, VSP_005049;
CC Name=PLEC-1D.2A;
CC IsoId=Q9QXS1-9; Sequence=VSP_005032, VSP_005041;
CC Name=PLEC-1B;
CC IsoId=Q9QXS1-10; Sequence=VSP_005032, VSP_005041, VSP_005048;
CC Name=PLEC-1E.2A;
CC IsoId=Q9QXS1-11; Sequence=VSP_005033;
CC Name=PLEC-1E;
CC IsoId=Q9QXS1-12; Sequence=VSP_005033, VSP_005042, VSP_005048;
CC Name=PLEC-1F;
CC IsoId=Q9QXS1-13; Sequence=VSP_005034, VSP_005043, VSP_005048;
CC Name=PLEC-1G;
CC IsoId=Q9QXS1-14; Sequence=VSP_005038, VSP_005046, VSP_005048;
CC Name=PLEC-1H;
CC IsoId=Q9QXS1-15; Sequence=VSP_005040;

CC Name=PLEC-11;
CC IsoId=Q9QXSI-16; Sequence=VSP_005035, VSP_005044;
CC TISSUE SPECIFICITY: Expressed at high levels in lung, brain, small
CC intestine, muscle, heart and skin with lower levels found in
CC kidney, liver, uterus, spleen and salivary gland.
CC -!- DOMAIN: The N-terminus interacts with actin, the C-terminus with
CC vimentin, desmin, GAP, cytochromes, lamin B; whereas both the N-
CC and the C-terminus can bind integrin beta-4.
CC -!- PTM: PHOSPHORYLATED BY CDC2; REGULATES DISSOCIATION FROM
CC INTERMEDIATE FILAMENTS DURING MITOSIS (BY SIMILARITY).
CC -!- SIMILARITY: Contains 1 actin-binding domain.
CC -!- SIMILARITY: Contains 2 calponin-homology (CH) domains.
CC -!- SIMILARITY: Contains 3 spectrin repeats.
CC -!- SIMILARITY: Belongs to the plakin or cytolinker family.
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CC -----
CC EMBL; AF188006; AAF18066.1; -;
CC EMBL; AF188007; AAF18067.1; -;
CC EMBL; AF188008; AAF18068.1; -;
CC EMBL; AF188009; AAF18069.1; -;
CC EMBL; AF188010; AAF18070.1; -;
CC EMBL; AF188011; AAF18071.1; -;
CC EMBL; AF188012; AAF18072.1; -;
CC EMBL; AF188013; AAF18073.1; -;
CC EMBL; AF188014; AAF18074.1; -;
CC EMBL; AF188015; AAF18075.1; -;
CC EMBL; AF188016; AAF18076.1; -;
CC EMBL; AF188017; AAF18077.1; -;
CC EMBL; AF188018; AAF18078.1; -;
CC EMBL; AF188019; AAF18079.1; -;
CC EMBL; AF188020; AAF18080.1; -;
CC EMBL; AF188021; AAF18081.1; -;
CC EMBL; AF188022; AAF18082.1; -;
CC EMBL; AF188023; AAF18083.1; -;
CC EMBL; AF188024; AAF18084.1; -;
CC MGD; MGI:1277961; Plect1.
CC InterPro; IPR001589; Actbind actinin.
CC InterPro; IPR001715; Calponin-like.
CC InterPro; IPR005346; S10_plectin_N.
CC InterPro; IPR002017; Spectrin.
CC Pfam; PF00307; CH; 2.
CC Pfam; PF03501; S10_plectin; 1.
CC Pfam; PF00435; spectrin; 2.
CC ProDom; PD006662; S10_plectin_N; 1.
CC ProSITE; PS00019; ACTININ_1; 1.
CC ProSITE; PS00020; ACTININ_2; FALSE_NEG.
CC ProSITE; PS00021; CH; 2.
CC Repeat; Structural protein; Cytoskeleton; Actin-binding;
KW Alternative splicing.
FT DOMAIN 1 >964 GLOBULAR.
FT DOMAIN 181 411 ACTIN-BINDING.
FT DOMAIN 185 293 CH 1.
FT DOMAIN 305 408 CH 2.
FT REPEAT 653 727 SPECTRIN 1.
FT REPEAT 748 832 SPECTRIN 2.
FT REPEAT 845 938 SPECTRIN 3.
FT VARSPLIC 1 5 MWAGM -> MKTVP (in isoform PLEC-1D and
FT isoform PLEC-1D,2A).
FT VARSPLIC 1 15 MWAGMPLDLRLAI -> MDPSRAIQHEISSLK (in
FT isoform PLEC-1E and isoform PLEC-1E,2A).
FT VARSPLIC 1 28 MWAGMPLDLRLAIYEVLFREGVWVAK -> MAHLITSGP
FT PDEQDFIQAYEVEKRYK (in isoform PLEC-1F).
FT VARSPLIC 1 33 MWAGMPLDLRLAIYEVLFREGVWVAKDRRP -> MNET

FT VARRKLSPGSGTNTLSRLRGTSVTCTKTS (in isoform
FT PLEC-1I).
FT /FTid=VSP_005035.
FT MWAGMPLDLRLAIYEVLFREGVWVAKDRRPRLSH ->
FT MSQRLRVPEPEGKSGKTSSEDNLYLAVLRASEGKK (in
FT isoform PLEC-1A).
FT /FTid=VSP_005036.
FT MWAGMPLDLRLAIYEVLFREGVWVAKDRRPRLSH ->
FT MEPSGSLFPLSLVVGHVVTIAAVHWKKGHROAKDEQ (in
FT isoform PLEC-1B and isoform PLEC-1B,2A).
FT /FTid=VSP_005037.
FT MWAGMPLDLRLAIYEVLFREGVWVAKDRRPRLSHPHVP
FT GVT -> MAGTWAARGVFTSQREVLLERPCWLDGCGEQVRR
FT GYLGLQCCV (in isoform PLEC-1G).
FT /FTid=VSP_005038.
FT MWAGMPLDLRLAIYEVLFREGVWVAKDRRPRLSHPHVP
FT GVTNLQVWRAWSLKARGLVRETF -> MSBEDSEVRPVA
FT VARGSSNGSGSPGDTLPWNLGKTORRRSGSGVNGS
FT VLDPAERAVIRIA (in isoform PLEC-0,1C,
FT isoform PLEC-0,1C,2A,3A and isoform
FT PLEC-0,1C,2A).
FT /FTid=VSP_005039.
FT Missing (in isoform PLEC-1H).
FT /FTid=VSP_005040.
FT Missing (in isoform PLEC-1D and isoform
FT PLEC-1D,2A).
FT /FTid=VSP_005041.
FT Missing (in isoform PLEC-1E).
FT /FTid=VSP_005042.
FT Missing (in isoform PLEC-1F).
FT /FTid=VSP_005043.
FT Missing (in isoform PLEC-1I).
FT /FTid=VSP_005044.
FT Missing (in isoform PLEC-1A, isoform
FT PLEC-1B and isoform PLEC-1B,2A).
FT /FTid=VSP_005045.
FT Missing (in isoform PLEC-1G).
FT /FTid=VSP_005046.
FT Missing (in isoform PLEC-0,1C and isoform
FT PLEC-0,1C,2A,3A).
FT /FTid=VSP_005047.
FT Missing (in isoform PLEC-1, isoform
FT PLEC-1,2A,3A).
Query Match 32.0%; Score 49; DB 1; Length 964;
Best Local Similarity 45.5%; Pred. No. 12;
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
QY 4 GRYKFKVQLDISIARLKTSMK 25
DB 733 GAYRDCLGRDLQYAKLNSK 754
RESULT 5
TOP2 CRIFA
ID TOP2 CRIFA STANDARD; PRT; 1239 AA.
AC F27570;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE DNA topoisomerase II (EC 5.99.1.3).
GN TOP2
OS Crithidia fasciculata.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Crithidia.
OX NCBI_TaxID=5656;
RN [1]
RP STRAIN=CFCI;
RX MEDLINE=9211798;
RA Pasion S.G., Hines J.C., Rebersold R., Ray D.S.;
RT "Molecular cloning and expression of the gene encoding the
RT kinetoplast-associated type II DNA topoisomerase of Crithidia
RT fasciculata."
RL Mol. Biochem. Parasitol. 50:57-68(1992).

```

CC CC -!- FUNCTION: Control of topological states of DNA by transient
CC CC breakage and subsequent rejoining of DNA strands. Topoisomerase II
CC CC makes double-strand breaks.
CC CC -!- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC CC of double-stranded DNA.
CC CC -!- SUBUNIT: Homodimer.
CC CC -!- SUBCELLULAR LOCATION: NUCLEAR AND KINETOPLAST.
CC CC -!- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both
CC CC negative and positive supercoils, whereas prokaryotic enzymes
CC CC relax only negative supercoils.
CC CC -!- SIMILARITY: Belongs to the type II topoisomerase family.
CC CC
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CC CC use by non-profit institutions as long as its content is in no way
CC CC modified and this statement is not removed. Usage by and for commercial
CC CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC CC or send an email to license@isb-sib.ch).
CC CC
CC CC EMBL; X59623; CAA42182.1; -.
CC CC DR PIR; A45648; A45648.
CC CC DR HSSP; P06786; 1BQW.
CC CC DR InterPro; IPR003594; ATPbind ATPase.
CC CC DR InterPro; IPR001241; DNA_topoisom.
CC CC DR InterPro; IPR002205; DNA_topoisomIV.
CC CC DR Pfam; PF00204; DNA_gyraseB; 1.
CC CC DR Pfam; PF00521; DNA_topoisomIV; 1.
CC CC DR PRINTS; PR00418; TP12FAMILY.
CC CC DR ProDom; PD000742; DNA_topoisomIV; 1.
CC CC DR SMART; SM00387; HATPase_C; 1.
CC CC DR SMART; SM00433; TOP2c; 1.
CC CC DR SMART; SM00434; TOP4c; 1.
CC CC DR PROSITE; PS00177; TOPOISOMERASE II; 1.
CC CC DR Komerase; Topoisomerase.
CC CC KW Kinetoplast; Mitochondrion.
CC CC FT ACT BIND 137 142 ATP (POTENTIAL).
CC CC FT NP SITE 137 775 DNA CLEAVAGE (BY SIMILARITY).
CC CC FT AC SITE 775 775 DNA CLEAVAGE (BY SIMILARITY).
CC CC SQ SEQUENCE 1239 AA; 138455 MW; 9FCB801382DDBD10 CRC64;

Query Match 32.0%; Score 49; DB 1; Length 1239;
Best Local Similarity 36.0%; Pred. No. 16;
Matches 9; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 5 RYRKFGQIDISIRLKTSMKPVKN 29
Db 999 RRTQIGLLEMDLARLQSTRFVEH 1023

RESULT 6
ID PLE1 HUMAN STANDARD; PRT; 4684 AA.
AC Q15149; Q15148; Q16640;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Plectin 1 (PLTN) (PCN) (Hemidesmosomal protein 1) (HD1).
GN PLE1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Placenta;
RX MEDLINE=96210632; PubMed=8633055;
RA Liu C.-G., Maercker C., Castanon M.J., Hauptmann R., Wiche G.;
RT "Human Plectin: organization of the gene, sequence analysis, and
RT chromosome localization. (8q24).";
RL Proc. Natl. Acad. Sci. U.S.A. 93:4278-4283 (1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), AND DISEASE.

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```

RX MEDLINE=96312447; PubMed=8698233;
RA McLean W.H.I., Pulkkinen L., Smith F.J.D., Rugg E.L., Lane E.B.,
RA Bullrich F., Burgess R.E., Amato S., Hudson D.L., Owaribe K.,
RA McGrath J.A., McWilliam J.R., Eady R.A.J., Leigh I.M., Cristiano A.M.,
RA Utito J.;
RT "Loss of plectin causes epidermolysis bullosa with muscular dystrophy:
RT cDNA cloning and genomic organization.";
RL Genes Dev. 10:1724-1735 (1996).
RN [3]
RP VARIANT MD-EBS 1003-GLN--ALA-1005 DEL.
RX MEDLINE=97049959; PubMed=8894687;
RA Pulkkinen L., Smith F.J.D., Shimizu H., Murata S., Yaoita H.,
RA Hachisuka H., Nishikawa T., McLean W.H.I., Utito J.;
RT "Homozygous deletion mutations in the plectin gene (PLEC1) in patients
RT with epidermolysis bullosa simplex associated with late-onset
RT muscular dystrophy.";
RN Hum. Mol. Genet. 5:1539-1546 (1996).
RN [4]
RP VARIANT MD-EBS LEU-429 INS.
RX MEDLINE=2109821; PubMed=11159198;
RA Bauer J.W., Rouan F., Kofler B., Resniczek G.A., Kornacker I.,
RA Wiche W., Hametner R., Klausegger A., Huber A., Pohla-Gubo G.,
RA Wiche G., Utito J., Hintner H.;
RT "A compound heterozygous one amino-acid insertion/nonsense mutation in
RT the plectin gene causes epidermolysis bullosa simplex with plectin
RT deficiency.";
RL Am. J. Pathol. 158:617-625 (2001).
RN [5]
RP VARIANT EBS1 TRP-2110.
RX MEDLINE=21841370; PubMed=11851880;
RA Koss-Harnes D., Hoeyheim B., Anton-Lamprecht I., Gjesti A.,
RA Joergensen R.S., Jahnson F.L., Olaisen B., Wiche G.,
RA Gedde-Dahl T. Jr.;
RT "A site-specific plectin mutation causes dominant epidermolysis
RT bullosa simplex Ogna: two identical de novo mutations.";
RL J. Invest. Dermatol. 118:87-93 (2002).
CC -!- FUNCTION: Interlinks intermediate filaments with microtubules and
CC microfilaments and anchors intermediate filaments to desmosomes or
CC hemidesmosomes. Could also bind muscle proteins such as actin to
CC membrane complexes in muscle. May be involved not only in the
CC crosslinking and stabilization of cytoskeletal intermediate
CC filaments network, but also in the regulation of their dynamics.
CC -!- SUBUNIT: Homodimer or homotetramer.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=Q15149-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q15149-2; Sequence=VSP_005030;
CC Name=3;
CC IsoId=Q15149-3; Sequence=VSP_005030, VSP_005031;
CC -!- TISSUE SPECIFICITY: Widely expressed with highest levels in
CC muscle, heart, placenta and spinal cord.
CC -!- DOMAIN: The N-terminus interacts with actin, the C-terminus with
CC vimentin, desmin, GFAP, cytokeratins, lamin B; whereas both the N-
CC and the C-terminus can bind integrin beta-4.
CC -!- PTM: PHOSPHORYLATED BY CDC2; REGULATES DISSOCIATION FROM
CC INTERMEDIATE FILAMENTS DURING MITOSIS (BY SIMILARITY).
CC -!- DISEASE: Defects in PLE1 are the cause of epidermolysis bullosa
CC simplex with muscular dystrophy (MD-EBS) [MIM:226670]; an
CC autosomal recessive disorder characterized by epidermal blister
CC formation at the level of the hemidesmosome and associated with
CC late-onset muscular dystrophy.
CC -!- DISEASE: Defects in PLE1 are the cause of epidermolysis bullosa
CC simplex 1 (EBS1) [MIM:131950]; also called epidermolysis bullosa
CC simplex Ogna type. EBS1 is an autosomal dominant form of
CC epidermolysis bullosa simplex differentiated from the more
CC generalized form of Koebner [MIM:131900] and the localized form of
CC Weber and Cockayne [MIM:131800] by the occurrence of skin
CC bruising.
CC -!- SIMILARITY: Contains 1 actin-binding domain.
CC -!- SIMILARITY: Contains 2 calponin-homology (CH) domains.
CC -!- SIMILARITY: Contains 33 plectin repeats.

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DE Fdhd protein homolog.
GN FDHD OR NARO OR MW2198.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=196620;
[1]
SEQUENCE FROM N.A.
MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
Yamamoto K., Hiranatsu K.;
RA "Genome and virulence determinants of high virulence community-
RRT acquired MRSA.";
RRL Lancet 359:1819-1827(2002).
CC -!- FUNCTION: Necessary for formate dehydrogenase activity (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: Belongs to the fdhd family.
CC
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CC
CC EMBL; AP004829; BAB96063.1; -.
CC HAWAP; MF_00187; -.
CC InterPro; IPR003786; Fdhd.
CC Pfam; PF02634; Fdhd-NaQ; 1.
CC TIGRFAMs; TIGR00129; fdhd_naQ; 1.
CC Complete proteome.
CC
CC SEQUENCE 265 AA; 29415 MW; 8186FFEBCE5072EB CRC64;
CC
Query Match 30.7%; Score 47; DB 1; Length 265;
Best Local Similarity 54.5%; Pred. No. 6.6;
Matches 12; Conservative 3; Mismatches 5; Indels 2; Gaps 1;
QY 3 CGRYKPFVGQLDISIARLKTSM 24
DB 107 CGKSRFQNDAAIA--KTSM 125
[1]
RESULT 10
CBP3_SCHPO STANDARD; PRT; 283 AA.
ID CBP3 SCHPO AC Q9USK6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE CBP3-like protein.
GN CBP3 OR SPC0433.17.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
[1]
SEQUENCE FROM N.A.
STRAIN=972;
RA MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gilliland R., Rajadream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDaniel S., McLean J.,
RA Mcneely P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford J., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.

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RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymoprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Carrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
RT "The genome sequence of Schizosaccharomyces pombe."
RL Nature 415:871-880(2002).
CC -!- SIMILARITY: Belongs to the CBP3 family.

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CC or send an email to license@isb-sib.ch).

CC EMBL; AL132870; CAB60691.1; -.
DR PIR; T50431; T50431.
DR GeneDB SPombe; SPOC4B3.17; -.
DR InterPro; IPR007129; Ubiquitin C chap.
DR Pfam; PF03981; Ubiquitin C chap; 1.
SQ SEQUENCE 2881 AA; 32972 MW; E32529E420029579 CRC64;

Query Match 30.7%; Score 47; DB 1; Length 283;
Best Local Similarity 40.0%; Pred. No. 7.1;
Matches 8; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 9 FVQGLDISIARLKTSMKFKV 28

DB 231 FVGRPDVLLVETIVKFR 250

RESULT 11

ID PANC COREF STANDARD; PRT; 287 AA.
AC Q8FUK6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pantoate-beta-alanine ligase (EC 6.3.2.1) (Pantothenate synthetase)
DE (Pantoate activating enzyme).
GN PANC OR CE0115.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RX MEDLINE=22723752; PubMed=12840036;
RA Nishio Y., Nakamura Y., Kawabayashi Y., Usuda Y., Kimura E.,
RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
RA Gojobori T.;
RT "Comparative complete genome sequence analysis of the amino acid
RT replacements responsible for the thermostability of Corynebacterium
RL Genome Res. 13:1572-1579(2003).
CC -!- CATALYTIC ACTIVITY: ATP + (R)-pantoate + beta-alanine = AMP +
CC diphosphate + (R)-pantothenate.
CC -!- PATHWAY: Pantothenate biosynthesis; last step.
CC -!- SIMILARITY: Belongs to the pantothenate synthetase family.
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CC EMBL; AP005214; BAC16925.1; ALT_INIT.
DR HAMAP; MF 00158; -; 1.
DR InterPro; IPR003721; Pantoate_ligase.
DR Pfam; PF02569; Pantoate_ligase; 1.
DR TIGRFAMs; TIGR00018; panC; 1.
KW Pantothenate biosynthesis; Ligase; Complete proteome.
SQ SEQUENCE 287 AA; 31266 MW; A5F813159627E7D1 CRC64;

Query Match 30.7%; Score 47; DB 1; Length 287;

Best Local Similarity 45.0%; Pred. No. 7.2;
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 DGGYRKVEGQLDISIARLK 21

DB 67 DDDYRNPYRQLDADVALLE 86

RESULT 12

FA10 RABIT

ID FA10 RABIT STANDARD; PRT; 490 AA.
AC O19045;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN F10.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9996;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97256311; PubMed=3101642;
RA Pendurthi U.R., Anderson K.D., James H.L.;
RT "Characterization of a full-length cDNA for rabbit factor X."
RL Thromb. Res. 85:503-514(1997).
CC -!- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
CC converts prothrombin to thrombin in the presence of factor Va,
CC calcium and phospholipid during blood clotting.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
CC Arg-|-Ile bonds in prothrombin to form thrombin.
CC -!- SUBUNIT: The two chains are formed from a single-chain precursor
CC by the excision of two Arg residues and are held together by 1 or
CC more disulfide bonds.
CC -!- PTM: The vitamin K-dependent, enzymatic carboxylation of some
CC glutamate residues allows the modified protein to bind calcium (By
CC similarity).
CC -!- PTM: N- and O-glycosylated (By similarity).
CC -!- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)
CC (BY SIMILARITY).
CC -!- MISCELLANEOUS: Calcium also binds, with stronger affinity to
CC another site, beyond the GLA domain.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 2 EGF-like domains.

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CC or send an email to license@isb-sib.ch).

CC EMBL; AF003200; AAB62542.1; -.

DR HSSP; P00742; 1HCG.

DR MEROPS; S01.216; -.

DR InterPro: IPR000152; Asx hydroxyl S.
 DR InterPro: IPR000003; Cys Ser trypsin.
 DR InterPro: IPR000742; EGF-2.
 DR InterPro: IPR001881; EGF-Ca.
 DR InterPro: IPR001438; EGF-II.
 DR InterPro: IPR006209; EGF-like.
 DR InterPro: IPR002383; GLA blood.
 DR InterPro: IPR001254; Peptidase S1.
 DR InterPro: IPR001314; Peptidase S1A.
 DR InterPro: IPR000294; Vitk_dep_GLA.
 DR Pfam: PF00008; EGF; 2.
 DR Pfam: PF00594; Gla; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PRO0722; CHYMOTRYPSIN.
 DR PRINTS: PRO0010; EGF-BLOOD.
 DR PRINTS: PRO0001; GLABLOOD.
 DR SMART: SMC00179; EGF_CA; 1.
 DR SMART: SMC00069; GLA; 1.
 DR SMART: SMC0020; TVP_SPC; 1.
 DR PROSITE: PS00010; ASX HYDROXYL; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS00026; EGF_3; 1.
 DR PROSITE: PS01187; EGF_CA; 1.
 DR PROSITE: PS00011; GLU CARBOXYLATION; 1.
 DR PROSITE: PS50240; TRYPSIN DOM; 1.
 DR PROSITE: PS00134; TRYPSIN HIS; 1.
 DR PROSITE: PS00135; TRYPSIN SER; 1.
 DR Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
 KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 KW Signal; Zymogen; EGF-like domain; Repeat.
 FT SIGNAL 1 20 POTENTIAL.
 FT PROPEP 21 40 BY SIMILARITY.
 FT CHAIN 41 180 FACTOR X LIGHT CHAIN.
 FT CHAIN 184 490 FACTOR X HEAVY CHAIN.
 FT PROPEP 184 232 ACTIVATION PEPTIDE.
 FT CHAIN 233 490 ACTIVATED FACTOR XA, HEAVY CHAIN.
 FT DOMAIN 86 122 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 125 165 EGF-LIKE 2.
 FT DOMAIN 233 490 SERINE PROTEASE.
 FT MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID (BY
 FT SIMILARITY).
 FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID (BY
 FT SIMILARITY).
 FT MOD_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID (BY
 FT SIMILARITY).
 FT MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID (BY
 FT SIMILARITY).
 FT MOD_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID (BY
 FT SIMILARITY).
 FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID (BY
 FT SIMILARITY).
 FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID (BY
 FT SIMILARITY).
 FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID (BY
 FT SIMILARITY).
 FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID (BY
 FT SIMILARITY).
 FT MOD_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID (BY
 FT SIMILARITY).
 FT MOD_RES 75 75 GAMMA-CARBOXYGLUTAMIC ACID (BY
 FT SIMILARITY).
 FT MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID (BY
 FT SIMILARITY).
 FT MOD_RES 103 103 HYDROXYLATION (BY SIMILARITY).
 FT ACT_SITE 274 274 CHARGE RELAY SYSTEM.
 FT ACT_SITE 320 320 CHARGE RELAY SYSTEM.
 FT ACT_SITE 417 417 CHARGE RELAY SYSTEM.
 FT DISULFID 90 101 BY SIMILARITY.
 FT DISULFID 95 110 BY SIMILARITY.
 FT DISULFID 112 121 BY SIMILARITY.
 FT DISULFID 129 140 BY SIMILARITY.
 FT DISULFID 136 149 BY SIMILARITY.

FT DISULFID 151 164 BY SIMILARITY.
 FT DISULFID 172 340 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 239 244 BY SIMILARITY.
 FT DISULFID 259 275 BY SIMILARITY.
 FT DISULFID 388 402 BY SIMILARITY.
 FT DISULFID 413 441 BY SIMILARITY.
 FT CARBOHYD 61 61 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 187 187 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 205 205 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 490 AA; 53965 MW; 3A39FA85AF2A6D11 CRC64;
 Query Match 30.4%; Score 46.5; DB 1; Length 490;
 Best Local Similarity 35.7%; Pred. No. 15;
 Matches 10; Conservative 8; Mismatches 7; Indels 3; Gaps 1;
 QY 5 RYKRVGQ---LDISARLKTKSMKPVKN 29
 DB 308 KHNREVKETDYDFDIADVLRLLKTPITFRN 335
 RESULT 13
 ID PANC_CORGL STANDARD; PRT; 279 AA.
 AC Q9X713;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Pantoate-beta-alanine ligase (EC 6.3.2.1) (Pantothenate synthetase)
 DE (Pantoate activating enzyme).
 DE PANC OR CG10113.
 GN Corynebacterium glutamicum (Brevibacterium flavum).
 OS Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TaxID:1718;
 RN [1]_SEQUENCE FROM N.A.
 RP STRAIN-ATCC 13032 / DSM 20300 / NCIB 10025;
 RC MEDLINE=99240418; PubMed=10223988;
 RA Eggeling L., Sahm H.;
 RT "D-pantothenate synthesis in Corynebacterium glutamicum and use of
 panBC and genes encoding L-valine synthesis for D-pantothenate
 overproduction.";
 RL Appl. Environ. Microbiol. 65:1973-1979(1999).
 RN [2]_SEQUENCE FROM N.A.
 RP STRAIN-ATCC 13032 / DSM 20300 / NCIB 10025;
 RC Nakagawa S.;
 RL "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: ATP + (R)-pantoate + beta-alanine = AMP +
 CC diphosphate + (R)-pantothenate.
 CC -!- PATHWAY: Pantothenate biosynthesis; last step.
 CC -!- SIMILARITY: Belongs to the pantothenate synthetase family.
 CC -----
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 CC -----
 CC EMBL; X96580; CAA65398.1; -.
 DR EMBL; AF005274; BAB97506.1; -.
 DR FIR; T47120; T47120.
 DR HAMAP; MF 00158; -; 1.
 DR InterPro; IPR003721; Pantoate_ligase.
 DR Pfam; PF02569; Pantoate_ligase; 1.
 DR TIGRFAMs; TIGR00018; panC; 1.
 KW Pantothenate biosynthesis; Ligase; Complete proteome.
 SQ SEQUENCE 279 AA; 29888 MW; EE4CF5EB4198A768 CRC64;
 Query Match 30.1%; Score 46; DB 1; Length 279;

Best Local Similarity 45.0%; Pred. No. 10;
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 DCGRYKRVGQLDISIARKL 21
|||:|:|:|:|:
DB 63 DCDYRNYPRQIDADLALLE 82

RESULT 14

LEUL CANBP
ID LEUL_CANBP STANDARD; PRT; 519 AA.
AC Q7VQJ6;
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE 2-isopropylmalate synthase (EC 2.3.3.13) (Alpha-isopropylmalate synthase) (Alpha-IPM synthetase).
GN LEUA OR BFL133.
OS Candidatus Blochmannia floridanus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; ant endosymbionts; Candidatus Blochmannia.
OX NCBI_TaxID=203907;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22784745; PubMed=12886019;
RA Gil R., Silva F.J., Zientz E., Delmotte F., Gonzalez-Candelas F.,
RA Latorre A., Rausell C., Kamerbeek J., Gadau J., Hoelldobler B.,
RA van Ham R.C.H.J., Gross R., Moya A.;
RT "The genome sequence of Blochmannia floridanus: comparative analysis of reduced genomes".
RL Proc. Natl. Acad. Sci. U.S.A. 100:9388-9393(2003).
CC -!- FUNCTION: Catalyzes the condensation of the acetyl group of acetyl-CoA with 3-methyl-2-oxobutanoate (2-oxoisovalerate) to form 3-carboxy-3-hydroxy-4-methylpentanoate (2-isopropylmalate).
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + 3-methyl-2-oxobutanoate + H(2)O = 2-hydroxy-2-isopropylsuccinate + CoA.
CC -!- PATHWAY: Leucine biosynthesis; first step.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SIMILARITY: Belongs to the alpha-IPM synthetase / homocitrate synthase family. LeuA 1 subfamily.
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CC
CC EMBL; BX248584; CAD83654.1; -;
CC HAMAP; MF 01025; -; 1.
CC InterPro; IPR002034; AIPM/Hcit_synth.
CC InterPro; IPR000891; HMGL-like.
CC InterPro; IPR005671; LeuA_bact_synth.
CC Pfam; PF00682; HMGL-like; 1.
CC TIGRFAMs; TIGR00973; leuA_bact; 1.
CC PROSITE; PS00815; AIPM_HOMOCIT_SYNTH_1; 1.
CC PROSITE; PS00816; AIPM_HOMOCIT_SYNTH_2; 1.
KW Leucine biosynthesis; Transferase; Complete proteome.
SQ SEQUENCE 519 AA; 58332 MW; 1E03737CEAD8FFD CRC84;

Query Match 30.1%; Score 46; DB 1; Length 519;
Best Local Similarity 38.5%; Pred. No. 19;
Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 CDCGRYKRVGQLDISIARKL 26
|||:|:|:|:|:
DB 69 CVCGLARCLEKDIDIAEALSAKKP 94

RESULT 15

YJ16 YEAST
ID YJ16_YEAST STANDARD; PRT; 604 AA.

P47112;
AC 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical 68.4 kDa protein in SSC1-HYP1 intergenic region.
GN YJR046W OR J1641.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=S288C;
RX MEDLINE=95397595; PubMed=7668047;
RA Huang M.-B., Chuat J.-C., Galibert F.;
RT "Analysis of a 42.5 kb DNA sequence of chromosome X reveals three tRNA genes and 14 new open reading frames including a gene most probably belonging to the family of ubiquitin-protein ligases.";
RL Yeast 11:775-781(1995).
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CC
CC EMBL; L36344; AAA88748.1; -;
CC EMBL; Z49546; CAA89574.1; -;
CC PIR; S57065; S57065.
CC GERMOnline; I41879; -;
CC SGD; S0003807; TAH11.
CC GO; GO:0005737; Cytoplasm; IDA.
CC GO; GO:0005634; C:nucleus; IDA.
CC GO; GO:0030174; P:DNA replication licensing; IDA.
KW Hypothetical protein.
SQ SEQUENCE 604 AA; 68405 MW; 099992C0B3CCA726 CRC64;

Query Match 30.1%; Score 46; DB 1; Length 604;
Best Local Similarity 60.0%; Pred. No. 22;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 14 DISTARLKTSMKFKV 28
:|:|:|:|:|:|:|:
DB 301 ELSILRLQDANKFKV 315

Search completed: March 8, 2004, 12:12:08
Job time : 5.59912 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:02:31 ; Search time 22.2291 Seconds
(without alignments)

411.624 Million cell updates/sec

Title: US-09-600-932-2_COPY_119_147

Perfect score: 153

Sequence: 1 CDCGRYKFKVQGLDISIARLKTSMKFKVN 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_todent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	153	100.0	277	4	Q9Y6Z7 homo sapien
2	144	94.1	277	11	Q8CF98
3	144	94.1	277	11	Q8CIC5
4	101	65.0	271	13	Q7T0T0 xenopus lae
5	83	54.2	272	11	Q9DC75
6	80	52.3	268	4	Q7Z6N1
7	80	52.3	271	4	Q8BWP8
8	55	35.9	71	7	Q9GJ67 salmo trutt
9	52	34.0	1454	13	Q7ZWNK4
10	50	32.7	282	12	Q9T1R4
11	50	32.7	1490	3	Q8TFJ9
12	49	32.0	149	16	Q884X4
13	49	32.0	188	2	Q45307 bacillus li
14	49	32.0	254	11	P70636
15	49	32.0	676	11	Q8C855
16	48.5	31.7	1236	5	Q9N8A4

17	48.5	31.7	1236	5	Q9XZN0
18	48	31.4	71	7	Q9GJ70
19	48	31.4	71	7	Q9GJ69
20	48	31.4	265	16	Q97MD7
21	48	31.4	276	2	Q83X29
22	48	31.4	426	12	Q8UZM4
23	48	31.4	465	16	Q9KSB6
24	48	31.4	607	16	Q9QYI6
25	48	31.4	1070	10	Q9LGH5
26	47.5	31.0	358	16	Q97KW4
27	47.5	31.0	1791	5	Q8IHK4
28	47	30.7	149	16	Q8DUZ2
29	47	30.7	191	16	Q92CQ8
30	47	30.7	420	16	Q825L5
31	47	30.7	639	16	Q883E2
32	46.5	30.4	136	2	O32829
33	46.5	30.4	581	10	Q9S7U7
34	46.5	30.4	797	5	Q9GV13
35	46	30.1	100	2	Q93I76
36	46	30.1	288	17	Q979I4
37	46	30.1	392	4	O8IVX0
38	46	30.1	400	4	Q14183
39	46	30.1	400	4	Q7ZSG0
40	46	30.1	403	11	P70611
41	46	30.1	405	11	O35527
42	46	30.1	405	11	Q7TNF0
43	46	30.1	447	16	Q9CJ29
44	46	30.1	452	5	Q9GVA1
45	46	30.1	459	3	P78720

ALIGNMENTS

RESULT 1

Q9Y6Z7 PRELIMINARY; PRT; 277 AA.

AC Q9Y6Z7; 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Collectin 34.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

ON NCBI_TaxID=9606;

OX [1]

RP SEQUENCE FROM N.A.

EX MEDLINE=99240768; PubMed=10224141;

RA Ohnishi K., Suzuki Y., Eda S., Kawai T., Kase T., Yamazaki H.,

RA Keshi H., Sakai Y., Fukuo A., Sakamoto T., Wakamiya N.;

RT "Molecular cloning of a novel collectin from liver (CL-L1).";

RL J. Biol. Chem. 274:13681-13689(1999).

DR EMBL; AB002631; BAA81747.1; -

DR HSSP; P19999; 2MSB.

DR Genew; HGNC:2220; COLC10.

DR GO; GO:0005737; C:cytoplasm; TAS.

DR GO; GO:0005530; F:lectin; TAS.

DR InterPro; IPR008160; Collagen.

DR InterPro; IPR001304; LECTIN_C.

DR Pfam; PF01391; Collagen; 1.

DR Pfam; PF00059; LECTIN_C; 1.

DR SMART; SM00034; CLACT1.

DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.

DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.

DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.

DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.

DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.

DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.

DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.

DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.

DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.

DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.

DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.

DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.

DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.

DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.

DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.

DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.

DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.

DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.

```
Db 119 CDCGRYKRVGQLDISARLKTSMKFKVN 147
RESULT 2
Q8CF98 PRELIMINARY; PRT; 277 AA.
AC Q8CF98;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Collectin-L1. (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=2233927; PubMed=1450124;
RA Kawai T., Suzuki Y., Eda S., Kase T., Ohtani K., Sakai Y., Keshi H.,
RA Fukuchi A., Sakamoto T., Nozaki M., Copeland N.G., Jenkins N.A.,
RA Wakamiya N.;
RT "Molecular Cloning of Mouse Collectin Liver 1.";
RL Biosci. Biotechnol. Biochem. 66:2134-2145(2002).
DR EMBL; AB018429; BAC53954.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 277 AA; 30524 MW; 98C743A2E07A2872 CRC64;

Query Match 94.1%; Score 144; DB 11; Length 277;
Best Local Similarity 89.7%; Pred. No. 1.6e-14;
Matches 26; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CDCGRYKRVGQLDISARLKTSMKFKVN 29
Db 119 CDCGRYKRVGQLDISVARLKTSMKFKVN 147

RESULT 3
Q8C1C5 PRELIMINARY; PRT; 277 AA.
AC Q8C1C5;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Collectin 34 homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK028423; BAC25941.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
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DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 277 AA; 30510 MW; 94EF23A2E5404872 CRC64;

Query Match 94.1%; Score 144; DB 11; Length 277;
Best Local Similarity 89.7%; Pred. No. 1.6e-14;
Matches 26; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CDCGRYKRVGQLDISARLKTSMKFKVN 29
Db 119 CDCGRYKRVGQLDISVARLKTSMKFKVN 147

RESULT 4
Q7TOT0 PRELIMINARY; PRT; 271 AA.
AC Q7TOT0;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.S., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Klein S., Strausberg R.;
RA Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056052; AAH56052.1; -.
KW Hypothetical protein.
SQ SEQUENCE 271 AA; 29334 MW; 587129273C476AE2 CRC64;

Query Match 66.0%; Score 101; DB 13; Length 271;
Best Local Similarity 58.6%; Pred. No. 1.1e-07;
Matches 17; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 CDCGRYKRVGQLDISARLKTSMKFKVN 29
Db 119 CDCGRYKRVGQLDISVARLKTSMKFKVN 147
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Db 113 CECGQLKXAVGEMDIQVAQLATEYKFKVN 141
RESULT 5
Q9DC75 PRELIMINARY; PRT; 272 AA.
AC Q9DC75 (1)
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE 101000IH16RIK protein.
GN 101000IH16RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata Y., Konno M., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kondo S., Yamataka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojocori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staib F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Roffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Rodriguez I., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayaishizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK003121; BAB22581.1; -.
DR HSSP; P22897; LEGG.
DR MGD; MGI:1918943; 101000IH16RIK.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; LECTIN_C.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF00059; lectin c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.
DR PROSITE; PS50041; C-TYPE LECTIN 2; 1.
SQ SEQUENCE 272 AA; 28975 MW; DE471493CD16B95 CRC64;

Query Match 54.2%; Score 83; DB 11; Length 272;
Best Local Similarity 41.4%; Pred. No. Be-05;
Matches 12; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 CDCGVRKFKVGQDLSIARLKTSMKFKVN 29
Db 114 CECGQLKXAVGEMDQVQTTLTFLKFN 142
RESULT 6
Q7Z6N1 PRELIMINARY; PRT; 268 AA.
AC Q7Z6N1 (1)
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE MGC3279 protein.
GN MGC3279.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC000078; AAH00078.1; -.
DR HSSP; P22897; LEGG.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; LECTIN_C.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF00059; lectin c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.
DR PROSITE; PS50041; C-TYPE LECTIN 2; 1.
SQ SEQUENCE 271 AA; 28665 MW; A14A248CE41DB340 CRC64;

Query Match 52.3%; Score 80; DB 4; Length 271;
Best Local Similarity 37.9%; Pred. No. 0.00024;
Matches 11; Conservative 11; Mismatches 7; Indels 0; Gaps 0;
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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klatner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bock S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009951; AAH09951.1; -.
SQ SEQUENCE 268 AA; 29005 MW; 30C30CC8258AA9B7 CRC64;

Query Match 52.3%; Score 80; DB 4; Length 268;
Best Local Similarity 37.9%; Pred. No. 0.00024;
Matches 11; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 1 CDCGVRKFKVGQDLSIARLKTSMKFKVN 29
Db 110 CECGQLKXAVGEMDQVQTLTFLKFN 138
RESULT 7
Q9BWP8 PRELIMINARY; PRT; 271 AA.
AC Q9BWP8 (1)
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC000078; AAH00078.1; -.
DR HSSP; P22897; LEGG.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; LECTIN_C.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF00059; lectin c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.
DR PROSITE; PS50041; C-TYPE LECTIN 2; 1.
KW Hypothetical protein.
SQ SEQUENCE 271 AA; 28665 MW; A14A248CE41DB340 CRC64;

Query Match 52.3%; Score 80; DB 4; Length 271;
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Best Local Similarity 37.9%; Pred. No. 0.00024;
Matches 11; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 1 CDCGRYKRVGQDLSIARLKTSMKFKVN 29
Db 113 CBCSOLRAIGMDNQVSLTSELAFIKN 141

RESULT 8
Q9GJ67 PRELIMINARY; PRT; 71 AA.
AC Q9GJ67;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE MHC class II alpha chain (Fragment).
GN SAIR-DA.
OS Salmo trutta (Brown trout).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8032;
RN [1]
RP SEQUENCE FROM N.A.
RA Stet R.J.M., Jordan W.C.;
RT "Class II alpha chain in brown trout (Salmo trutta).";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR ENBL; AJ293954; CAC08191.1;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001003; MHC_II_alpha.
DR Pfam; PF00993; MHC_II_alpha; 1.
FT NON TER 1
FT 71
SQ SEQUENCE 71 AA; 7667 MW; C00A0CCA0708BE80 CRC64;

Query Match 35.9%; Score 55; DB 7; Length 71;
Best Local Similarity 46.2%; Pred. No. 0.56;
Matches 12; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 4 GRYKRVGQDLSIARLKTSMKFKVN 29
Db 43 GAVEQAVGELGVCKANLATSIKAYKN 68

RESULT 9
Q7ZWK4 PRELIMINARY; PRT; 1454 AA.
AC Q7ZWK4;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Similar to plectin (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC048220; AAH48220.1;
DR GO; GO:0003779; F:actin binding; IEA.
DR InterPro; IPR001589; Actbind actinin.
DR InterPro; IPR001715; Calponin-like.
DR InterPro; IPR002017; Spectrin.
DR Pfam; PF00307; Ch; 2.
DR Pfam; PF00435; spectrin; 1.
DR SMART; SM00033; CH; 2.
DR SMART; SM00150; SPEC; 5.
DR PROSITE; PS00019; ACTININ_1; 1.

DR PROSITE; PS00021; CH; 2.
FT NON TER 1454 1454
SQ SEQUENCE 1454 AA; 170240 MW; EA3DDB6ECD3BDAC9 CRC64;
Query Match 34.0%; Score 52; DB 13; Length 1454;
Best Local Similarity 40.9%; Pred. No. 41;
Matches 9; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 4 GRYKRVGQDLSIARLKTSMK 25
Db 590 GSYQVYLGKLDLQYAKLNSK 611

RESULT 10
Q91TR4 PRELIMINARY; PRT; 282 AA.
AC Q91TR4;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
DE T29.3.
OS Tupaia herpesvirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae.
OX NCBI_TaxID=10397;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2;
RX MEDLINE=21211637; PubMed=11312357;
RA Bahr U., Darai G.;
RT "Analysis and Characterization of the Complete Genome of Tupaia (Tree Shrew) Herpesvirus.";
RL J. Virol. 75:4854-4870(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=2;
RA Darai G., Bahr U.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF281817; AAK57073.1;
SQ SEQUENCE 282 AA; 28737 MW; 6166B8DBF7981864 CRC64;

Query Match 32.7%; Score 50; DB 12; Length 282;
Best Local Similarity 39.1%; Pred. No. 15;
Matches 9; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 6 YRKRVGQDLSIARLKTSMKFKV 28
Db 209 WAEFFGKCSLSIARLKGFEYK 231

RESULT 11
Q8TFJ9 PRELIMINARY; PRT; 1490 AA.
AC Q8TFJ9;
DT 01-JUN-2002 (TREMELrel. 21, Created)
DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Polypyrroline.
GN GAG.
OS Debaryomyces hansenii var. hansenii.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
OX NCBI_TaxID=58641;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767; TRANSPOSON=LTR-retrotransposon Tdh5;
RA Neuveglise C., Feldmann H., Bon E., Gaillardin C., Casaregola S.;
RT "Genomic evolution of the LTR-retrotransposons in hemiascomycetous yeasts.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL; AJ439552; CAD29538.1;
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.


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DR GO: GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0006310; P:DNA recombination; IEA.
DR GO: GO:0006278; P:RNA dependent DNA replication; IEA.
DR InterPro: IPR001584; RvE.
DR InterPro: IPR000477; RVtse.
DR InterPro: IPR001878; Znf_CCHC.
DR Pfam: PF00665; rve; 1.
DR Pfam: PF00078; rvt; 1.
DR Pfam: PF00098; zf_CCHC; 1.
DR PRINTS; PR00939; C2HCZNFINGER.
DR SMART; SM00343; Znf_C2HC; 1.
DR PROSITE; PS0158; ZF_CCHC; 1.
KW RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 1490 AA; 166461 MW; 2EALB73403FC967B CRC64;

Query Match 32.7%; Score 50; DB 3; Length 1490;
Best Local Similarity 34.6%; Pred.No. 88;
Matches 9; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 CDCGRYKRVGQLDISIALRLKTSMKF 26
   ||||| ||| : : : :
Db 1262 CDATYRSLVGKLPASTVTRTDIAY 1287

RESULT 12
Q884X4 PRELIMINARY; PRT; 149 AA.
AC Q884X4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Flagellar protein FljJ, putative.
GN PSPT01962.
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RA Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
RA Berry K., Utterback T., Van Aken S., Feldblyum T., Gwin M.,
RA Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
RA Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidson T.,
RA White O., Fraser C., Collier A.;
RT "Complete sequence of Pseudomonas syringae";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB016862; AAO55480.1; -.
DR TIGR; PSPT01962; -.
KW Complete proteome.
SQ SEQUENCE 149 AA; 17515 MW; 210720F49E407291 CRC64;

Query Match 32.0%; Score 49; DB 16; Length 149;
Best Local Similarity 34.6%; Pred.No. 11;
Matches 8; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 6 YRKRVGQLDISIALRLKTSMKFVK 28
   ||||| ||| : : : :
Db 71 YQRFSLQDVAVAQYKSLWEHK 93

RESULT 13
Q45307 PRELIMINARY; PRT; 188 AA.
AC Q45307;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Saz divB (Fragment).
OS Bacillus licheniformis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1402;
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RN SEQUENCE FROM N.A.
RP STRAIN=5A2;
RX MEDLINE=94374713; PubMed=8088553;
RA Harry E.J., Partridge S.R., Weiss A.S., Wake R.G.;
RT "Conservation of the 188 divB gene in Bacillus subtilis W23 and B.
RT licheniformis, and evidence for homology to ftsQ of Escherichia
RT coli.";
RL Gene 147:85-89(1994).
DR EMBL; U01958; AAA57245.1; -.
DR PIR; I40222; I40222.
FT NON_TER 188
SQ SEQUENCE 188 AA; 21681 MW; 7D544902412E1774 CRC64;

Query Match 32.0%; Score 49; DB 2; Length 188;
Best Local Similarity 37.5%; Pred.No. 14;
Matches 9; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 2 DCGRYKRVGQLDISIALRLKTSMK 25
   ||||| ||| : : : :
Db 90 DVERYRMFVGEIGVQGEIGIKVTLK 113

RESULT 14
P70636 PRELIMINARY; PRT; 254 AA.
AC P70636;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Laminin chain (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=Buffalo; TISSUE=Liver;
RX MEDLINE=98085771; PubMed=9417868;
RA Seebacher T., Medina J.L., Bade B.G.;
RT "Laminin alpha5, a major transcript of normal and malignant rat liver
RT epithelial cells, is differentially expressed in developing and adult
RT liver.";
RL Exp. Cell Res. 237:70-76(1997).
DR EMBL; Y08882; CAA70093.1; -.
DR InterPro; IPR008985; ConA_like_1ec_g1.
FT NON_TER 1
FT NON_TER 254
SQ SEQUENCE 254 AA; 27708 MW; 68C5837F7E83414E CRC64;

Query Match 32.0%; Score 49; DB 11; Length 254;
Best Local Similarity 43.5%; Pred.No. 19;
Matches 10; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 4 GRYKRVGQLDISIALRLKTSMKF 26
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Db 97 GRVKRLIAQARSANKVSKMF 119

RESULT 15
Q8C8S5 PRELIMINARY; PRT; 676 AA.
AC Q8C8S5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Plectin 1 (Fragment).
GN PLEC1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE FROM N.A.
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RP SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6J; TISSUE=Retina;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573 (2002).
RL EMBL; AK044559; BAC31980.1; -.
DR MGD; MGI:1277961; Plecl.
DR GO; GO:003779; F-actin binding; IEA.
DR InterPro; IPR001599; Actbind_actinin.
DR InterPro; IPR001715; Calponin-like.
DR InterPro; IPR002017; Spectrin.
DR Pfam; PF03037; CH; 2.
DR SMART; SM00033; CH; 2.
DR SMART; SM0150; SPEC; 1.
DR PROSITE; PS00019; ACTININ_1; 1.
DR PROSITE; PS0021; CH; 2.
FT NON_TER 676
SQ SEQUENCE 676 AA; 77580 MW; 6DA7D8815CAB6C70 CRC64;

Query Match 32.0%; Score 49; DB 11; Length 676;
Best Local Similarity 45.5%; Pred. No. 55;
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 4 GYRKFVGQDISIAELKTSMK 25
DB 631 GAYRDCLGREDLQYAKLNSK 652

Search completed: March 8, 2004, 12:15:13
Job time : 23.2291 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:11:31 ; Search time 10.4758 Seconds
(without alignments)
584.534 Million cell updates/sec

Title: US-09-600-932-2_COPY_119_147

Perfect score: 153
Sequence: 1 CDCGRYKFKVGLDISIARLTKSMKFKVN 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	153	100.0	159	14	US-10-258-105-14
2	153	100.0	277	9	US-09-978-295A-97
3	153	100.0	277	9	US-09-978-697-97
4	153	100.0	277	9	US-09-978-132A-97
5	153	100.0	277	9	US-09-999-832A-97
6	153	100.0	277	10	US-09-978-189-97
7	153	100.0	277	10	US-09-978-608A-97
8	153	100.0	277	10	US-09-978-585A-97
9	153	100.0	277	10	US-09-978-191A-97
10	153	100.0	277	10	US-09-978-403A-97
11	153	100.0	277	10	US-09-978-564A-97
12	153	100.0	277	10	US-09-999-833A-97
13	153	100.0	277	10	US-09-981-915A-97
14	153	100.0	277	10	US-09-978-824-97
15	153	100.0	277	10	US-09-918-585A-97

16	153	100.0	277	10	US-09-978-423A-97	Sequence 97, Appl
17	153	100.0	277	10	US-09-978-193A-97	Sequence 97, Appl
18	153	100.0	277	10	US-09-999-830A-97	Sequence 97, Appl
19	153	100.0	277	10	US-09-978-757A-97	Sequence 97, Appl
20	153	100.0	277	10	US-09-978-187B-97	Sequence 97, Appl
21	153	100.0	277	10	US-09-978-643A-97	Sequence 97, Appl
22	153	100.0	277	10	US-09-978-375A-97	Sequence 97, Appl
23	153	100.0	277	10	US-09-978-298A-97	Sequence 97, Appl
24	153	100.0	277	10	US-09-978-188A-97	Sequence 97, Appl
25	153	100.0	277	10	US-09-978-681A-97	Sequence 97, Appl
26	153	100.0	277	10	US-09-978-194A-97	Sequence 97, Appl
27	153	100.0	277	10	US-09-999-823A-97	Sequence 97, Appl
28	153	100.0	277	10	US-09-978-299A-97	Sequence 97, Appl
29	153	100.0	277	10	US-09-978-544A-97	Sequence 97, Appl
30	153	100.0	277	10	US-09-978-665A-97	Sequence 97, Appl
31	153	100.0	277	10	US-09-978-802A-97	Sequence 97, Appl
32	153	100.0	277	13	US-10-053-586-100	Sequence 100, App
33	153	100.0	277	14	US-10-174-590-100	Sequence 100, App
34	153	100.0	277	14	US-10-176-758-100	Sequence 100, App
35	153	100.0	277	14	US-10-175-737-100	Sequence 100, App
36	153	100.0	277	14	US-10-173-706-100	Sequence 100, App
37	153	100.0	277	14	US-10-175-738-100	Sequence 100, App
38	153	100.0	277	14	US-10-175-752-100	Sequence 100, App
39	153	100.0	277	14	US-10-176-482-100	Sequence 100, App
40	153	100.0	277	14	US-10-176-757-100	Sequence 100, App
41	153	100.0	277	14	US-10-176-913-100	Sequence 100, App
42	153	100.0	277	14	US-10-180-552-100	Sequence 100, App
43	153	100.0	277	14	US-10-180-557-100	Sequence 100, App
44	153	100.0	277	14	US-10-173-700-100	Sequence 100, App
45	153	100.0	277	14	US-10-174-572-100	Sequence 100, App

ALIGNMENTS

RESULT 1

US-10-258-105-14
; Sequence 14, Application US/10258105
; Publication No. US20030158382A1
; GENERAL INFORMATION:
; APPLICANT: Wakamiya et al.
; TITLE OF INVENTION: No. US20030158382A1 Collectin
; FILE REFERENCE: 19036/38785
; CURRENT APPLICATION NUMBER: US/10/258,105
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: PCT/JP01/03468
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: JP 2000-120358
; PRIOR FILING DATE: 2000-04-21
; NUMBER OF SEQ ID NOS: 61
; SEQ ID NO 14
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Known CRD amino acid sequence of reported CL-L1 which was employed for searching EST data base.
US-10-258-105-14

Query Match 100.0%; Score 153; DB 14; Length 159;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCGRYKFKVGLDISIARLTKSMKFKVN 29

DB 1 CDCGRYKFKVGLDISIARLTKSMKFKVN 29

RESULT 2

US-09-978-295A-97
; Sequence 97, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCES: P2630P1C11
 CURRENT APPLICATION NUMBER: US/09/978,295A
 CURRENT FILING DATE: 2001-10-15
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/064249
 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066364
 PRIOR FILING DATE: 1997-11-21
 PRIOR APPLICATION NUMBER: 60/077450
 PRIOR FILING DATE: 1998-03-10
 PRIOR APPLICATION NUMBER: 60/077632
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077641
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077649
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077791
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 PRIOR APPLICATION NUMBER: 60/078004
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 PRIOR APPLICATION NUMBER: 60/079656
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 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079663
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079728

APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC27
CURRENT APPLICATION NUMBER: US/09/978,697
PRIOR FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
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PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30

Query Match 100.0%; Score 153; DB 9; Length 277;
Best Local Similarity 100.0%; Pred. No. 2e-16; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 29; Conservative 0;

1 CDCGRYKFKVQGLDSTARLKTSMKFKVN 29
119 CDCGRYKFKVQGLDSTARLKTSMKFKVN 147

RESULT 3
JS-09-978-697-97
Sequence 97 Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen

1	PRIOR APPLICATION NUMBER: 60/080105
2	PRIOR FILING DATE: 1998-03-31
3	PRIOR APPLICATION NUMBER: 60/080107
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72	PRIOR FILING DATE: 1998-04-29
73	PRIOR APPLICATION NUMBER: 60/083500

1	PRIOR FILING DATE: 1998-04-29	
2	PRIOR APPLICATION NUMBER: 60/083742	
3	PRIOR FILING DATE: 1998-04-30	
4	PRIOR APPLICATION NUMBER: 60/084366	
5	PRIOR FILING DATE: 1998-05-05	
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16	PRIOR APPLICATION NUMBER: 60/084598	
17	PRIOR FILING DATE: 1998-05-07	
18	PRIOR APPLICATION NUMBER: 60/084600	
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30	PRIOR APPLICATION NUMBER: 60/085582	
31	PRIOR FILING DATE: 1998-05-15	
32	PRIOR APPLICATION NUMBER: 60/085700	
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35	PRIOR FILING DATE: 1998-05-15	
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38	PRIOR APPLICATION NUMBER: 60/085580	
39	PRIOR FILING DATE: 1998-05-15	
40	PRIOR APPLICATION NUMBER: 60/085573	
41	PRIOR FILING DATE: 1998-05-15	
42	PRIOR APPLICATION NUMBER: 60/085704	
43	PRIOR FILING DATE: 1998-05-15	
44	PRIOR APPLICATION NUMBER: 60/085697	

Query Match 100.0%; Score 153; DB 9; Length 277;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 29: Conservative 0; Mismatches 0; Indels

QY 1 CDCGRRYKFGVQLDISIARLKTSMKFVK 29
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Db 119 CDCGRRYKFGVQLDISIARLKTSMKFVK 147

RESULT 4
US-09-378-192A-97
Sequence 97, Application US/09978192A
Patent No. US2002017553A1
GENERAL INFORMATION:
APPLICANT: Askenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bockstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Garbar, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunes, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P26301C9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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1 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 153; DB 9; Length 277;

Best Local Similarity 100.0%; Pred. No. 2e-16;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDGGRKFKVQGLDISIARLTKSMKFKVN 29
Db 119 CDGGRKFKVQGLDISIARLTKSMKFKVN 147

RESULT 5

US-09-999-832A-97

Sequence 97, Application US/09999832A

Publication No. US20020192706A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC63
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CDCGRYKFGQLDISIARLKTSMKFVN 29
Db 119 CDCGRYKFGQLDISIARLKTSMKFVN 147
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RESULT 6
US-09-978-189-97
; Sequence 97, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
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; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: P2630P1C7
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Query Match 100.0%; Score 153; DB 10; Length 277;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCGRYKFKVQGLDISIARLKTSMKFVKV 29
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RESULT 7

US-09-978-608A-97
; Sequence 97, Application US/09978608A
; Publication No. US20030045462A1

GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Baker Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnovers, Luc
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleon
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Kuo, Sophia S.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James;
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2630PIC22
;; CURRENT APPLICATION NUMBER: US/09/978,608A
;; NUMBER OF SEQ ID NOS: 624
;; Prior Application removed - See File Wrapper or Palm
;; SEQ ID NO 97

;; LENGTH: 277

;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-978-608A-97

Query Match 100.0%; Score 153; DB 10; Length 277;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCGRYKFKVQGLDISIARLKTSMKFVKV 29
Db 119 CDCGRYKFKVQGLDISIARLKTSMKFVKV 147

RESULT 8

US-09-978-585A-97
; Sequence 97, Application US/09978585A
; Publication No. US20030049633A1

GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Baker Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnovers, Luc
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleon
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Kuo, Sophia S.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James;
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2630PIC15
;; CURRENT APPLICATION NUMBER: US/09/978,585A
;; NUMBER OF SEQ ID NOS: 624
;; Prior Application removed - See File Wrapper or Palm
;; SEQ ID NO 97

;; LENGTH: 277

;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-978-585A-97

Query Match 100.0%; Score 153; DB 10; Length 277;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCGRYKFKVQGLDISIARLKTSMKFVKV 29
Db 119 CDCGRYKFKVQGLDISIARLKTSMKFVKV 147

RESULT 9

US-09-978-191A-97
; Sequence 97, Application US/09978191A
; Publication No. US20030050239A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi	PRIOR FILING DATE: 1998-03-27
APPLICANT: Baker Kevin P.	PRIOR APPLICATION NUMBER: 60/079786
APPLICANT: Botstein, David	PRIOR FILING DATE: 1998-03-27
APPLICANT: Desnoyers, Luc	PRIOR APPLICATION NUMBER: 60/079920
APPLICANT: Eaton, Dan	PRIOR FILING DATE: 1998-03-30
APPLICANT: Ferrara, Napoleon	PRIOR APPLICATION NUMBER: 60/079923
APPLICANT: Filvaroff, Ellen	PRIOR FILING DATE: 1998-03-30
APPLICANT: Fong, Sherman	PRIOR APPLICATION NUMBER: 60/080105
APPLICANT: Gao, Wei-Qiang	PRIOR FILING DATE: 1998-03-31
APPLICANT: Gerber, Hanspeter	PRIOR APPLICATION NUMBER: 60/080107
APPLICANT: Gerritsen, Mary E.	PRIOR FILING DATE: 1998-03-31
APPLICANT: Goddard, Audrey	PRIOR APPLICATION NUMBER: 60/080165
APPLICANT: Godowski, Paul J.	PRIOR FILING DATE: 1998-03-31
APPLICANT: Grimaldi, J. Christopher	PRIOR APPLICATION NUMBER: 60/080194
APPLICANT: Gurney, Kenneth L.	PRIOR FILING DATE: 1998-03-31
APPLICANT: Hillan, Kenneth J	PRIOR APPLICATION NUMBER: 60/080327
APPLICANT: Kijavin, Ivar J.	PRIOR FILING DATE: 1998-04-01
APPLICANT: Kuo, Sophia S.	PRIOR APPLICATION NUMBER: 60/080328
APPLICANT: Napier, Mary A.	PRIOR FILING DATE: 1998-04-01
APPLICANT: Pan, James	PRIOR APPLICATION NUMBER: 60/080333
APPLICANT: Paoni, Nicholas F.	PRIOR FILING DATE: 1998-04-01
APPLICANT: Roy, Margaret Ann	PRIOR APPLICATION NUMBER: 60/080334
APPLICANT: Shelton, David L.	PRIOR FILING DATE: 1998-04-01
APPLICANT: Stewart, Timothy A.	PRIOR APPLICATION NUMBER: 60/081070
APPLICANT: Tumas, Daniel	PRIOR FILING DATE: 1998-04-08
APPLICANT: Williams, P. Mickey	PRIOR APPLICATION NUMBER: 60/081049
APPLICANT: Wood, William I.	PRIOR FILING DATE: 1998-04-08
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic	
ACIDS Encoding the Same	
FILE REFERENCE: P2630PIC4	
CURRENT APPLICATION NUMBER: US/09/978,191A	
CURRENT FILING DATE: 2001-10-15	
PRIOR APPLICATION NUMBER: 09/918585	
PRIOR FILING DATE: 2001-07-30	
PRIOR APPLICATION NUMBER: 60/062250	
PRIOR FILING DATE: 1997-10-17	
PRIOR APPLICATION NUMBER: 60/064249	
PRIOR FILING DATE: 1997-11-03	
PRIOR APPLICATION NUMBER: 60/065311	
PRIOR FILING DATE: 1997-11-13	
PRIOR APPLICATION NUMBER: 60/066364	
PRIOR FILING DATE: 1997-11-21	
PRIOR APPLICATION NUMBER: 60/077450	
PRIOR FILING DATE: 1998-03-10	
PRIOR APPLICATION NUMBER: 60/077632	
PRIOR FILING DATE: 1998-03-11	
PRIOR APPLICATION NUMBER: 60/077641	
PRIOR FILING DATE: 1998-03-11	
PRIOR APPLICATION NUMBER: 60/077649	
PRIOR FILING DATE: 1998-03-11	
PRIOR APPLICATION NUMBER: 60/077791	
PRIOR FILING DATE: 1998-03-12	
PRIOR APPLICATION NUMBER: 60/078004	
PRIOR FILING DATE: 1998-03-13	
PRIOR APPLICATION NUMBER: 60/078886	
PRIOR FILING DATE: 1998-03-20	
PRIOR APPLICATION NUMBER: 60/078936	
PRIOR FILING DATE: 1998-03-20	
PRIOR APPLICATION NUMBER: 60/078910	
PRIOR FILING DATE: 1998-03-20	
PRIOR APPLICATION NUMBER: 60/078939	
PRIOR FILING DATE: 1998-03-20	
PRIOR APPLICATION NUMBER: 60/079294	
PRIOR FILING DATE: 1998-03-25	
PRIOR APPLICATION NUMBER: 60/079656	
PRIOR FILING DATE: 1998-03-26	
PRIOR APPLICATION NUMBER: 60/079664	
PRIOR FILING DATE: 1998-03-27	
PRIOR APPLICATION NUMBER: 60/079689	
PRIOR FILING DATE: 1998-03-27	
PRIOR APPLICATION NUMBER: 60/079663	
PRIOR FILING DATE: 1998-03-27	
PRIOR APPLICATION NUMBER: 60/079728	

APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C17
CURRENT APPLICATION NUMBER: US/09/978,403A
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30

Query Match 100.0%; Score 153; DB 10; Length 277;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y 1 CDCGRRKFGQLDISIARLTKTSMKFKVN 29
3b 119 CDCGRRKFGQLDISIARLTKTSMKFKVN 147

RESULT 10
JS-09-978-403A-97
Sequence 97, Application US/09978403A
Publication No. US2003050240A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen

;; PRIOR APPLICATION NUMBER: 60/080105
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080107
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080165
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080194
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080327
;; PRIOR FILING DATE: 1998-04-01
;; PRIOR APPLICATION NUMBER: 60/080328
;; PRIOR FILING DATE: 1998-04-01
;; PRIOR APPLICATION NUMBER: 60/080333
;; PRIOR FILING DATE: 1998-04-01
;; PRIOR APPLICATION NUMBER: 60/080334
;; PRIOR FILING DATE: 1998-04-01
;; PRIOR APPLICATION NUMBER: 60/081070
;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/081049
;; PRIOR FILING DATE: 1998-04-09
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;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/081195
;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/081203
;; PRIOR FILING DATE: 1998-04-09
;; PRIOR APPLICATION NUMBER: 60/081229
;; PRIOR FILING DATE: 1998-04-09
;; PRIOR APPLICATION NUMBER: 60/081955
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/081817
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/081819
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/081952
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/081838
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/082568
;; PRIOR FILING DATE: 1998-04-21
;; PRIOR APPLICATION NUMBER: 60/082569
;; PRIOR FILING DATE: 1998-04-21
;; PRIOR APPLICATION NUMBER: 60/082704
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082804
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082700
;; PRIOR FILING DATE: 1998-04-22
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;; PRIOR APPLICATION NUMBER: 60/082796
;; PRIOR FILING DATE: 1998-04-23
;; PRIOR APPLICATION NUMBER: 60/083336
;; PRIOR FILING DATE: 1998-04-27
;; PRIOR APPLICATION NUMBER: 60/083322
;; PRIOR FILING DATE: 1998-04-28
;; PRIOR APPLICATION NUMBER: 60/083392
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083495
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083496
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083499
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083545
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;; PRIOR APPLICATION NUMBER: 60/083558
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083559
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083500

;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083742
;; PRIOR FILING DATE: 1998-04-30
;; PRIOR APPLICATION NUMBER: 60/084366
;; PRIOR FILING DATE: 1998-05-05
;; PRIOR APPLICATION NUMBER: 60/084414
;; PRIOR FILING DATE: 1998-05-06
;; PRIOR APPLICATION NUMBER: 60/084441
;; PRIOR FILING DATE: 1998-05-06
;; PRIOR APPLICATION NUMBER: 60/084637
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084639
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084640
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084598
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084627
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;; PRIOR FILING DATE: 1998-05-07
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 153; DB 10; Length 277;
Best Local Similarity 100.0%; Pred. No. 2e-16; Indels 0; Gaps 0;
Matches 29; Conservative 0; Mismatches 0

QY 1 CDCGRYKFCQDLSIARLKTSMKFKVN 29
Db 119 CDCGRYKFCQDLSIARLKTSMKFKVN 147

RESULT 11
US-09-978-564A-97
; Sequence 97, Application US/09978564A
; Publication No. US20030050241A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kiljan, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C25
CURRENT APPLICATION NUMBER: US/09/978,564A
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
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PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
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PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
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PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
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PRIOR APPLICATION NUMBER: 60/079294
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PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
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PRIOR FILING DATE: 1998-03-30
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PRIOR FILING DATE: 1998-03-31
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PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
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PRIOR FILING DATE: 1998-04-22
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PRIOR FILING DATE: 1998-04-23
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PRIOR FILING DATE: 1998-04-27
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PRIOR FILING DATE: 1998-04-28
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PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06

[illegible]

;; PRIOR APPLICATION NUMBER: 60/080334
;; PRIOR FILING DATE: 1998-04-01
;; PRIOR APPLICATION NUMBER: 60/081070
;; PRIOR FILING DATE: 1998-04-08
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;; PRIOR FILING DATE: 1998-04-08
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;; PRIOR FILING DATE: 1998-04-21
;; PRIOR APPLICATION NUMBER: 60/082704
;; PRIOR FILING DATE: 1998-04-22
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;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082700
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082797
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082796
;; PRIOR FILING DATE: 1998-04-23
;; PRIOR APPLICATION NUMBER: 60/083336
;; PRIOR FILING DATE: 1998-04-27
;; PRIOR APPLICATION NUMBER: 60/083322
;; PRIOR FILING DATE: 1998-04-28
;; PRIOR APPLICATION NUMBER: 60/083392
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083495
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083496
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083499
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;; PRIOR FILING DATE: 1998-04-29
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;; PRIOR FILING DATE: 1998-04-29
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;; PRIOR FILING DATE: 1998-05-06
;; PRIOR APPLICATION NUMBER: 60/084637
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084639
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084640

;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084598
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084627
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;; PRIOR APPLICATION NUMBER: 60/084643
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/085339
;; PRIOR FILING DATE: 1998-05-13
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;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 153; DB 10; Length 277;

Best Local Similarity 100.0%; Pred. No. 28-16; Indels 0; Gaps 0;
Matches 29; Conservative 0; Mismatches 0;

Oy 1 CDCGRYKFKVQGLDISIARLKTSMKFKVN 29
Db 119 CDCGRYKFKVQGLDISIARLKTSMKFKVN 147

RESULT 13

US-09-981-915A-97
; Sequence 97, Application US/09981915A
; Publication No. US20030054986A1

GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Baker Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleon
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Kijavin, Ivar J.
;; APPLICANT: Kuo, Sophia S.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pao, James;
;; APPLICANT: Pao, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: P2630PIC12
;; CURRENT APPLICATION NUMBER: US/09/981.915A
;; CURRENT FILING DATE: 2001-10-16
;; PRIOR APPLICATION NUMBER: 09/918585
;; PRIOR FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/064249
;; PRIOR FILING DATE: 1997-11-03
;; PRIOR APPLICATION NUMBER: 60/065311
;; PRIOR FILING DATE: 1997-11-13
;; PRIOR APPLICATION NUMBER: 60/066364
;; PRIOR FILING DATE: 1997-11-21
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;; PRIOR FILING DATE: 1998-03-11
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;; PRIOR FILING DATE: 1998-03-11
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;; PRIOR FILING DATE: 1998-03-12
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;; PRIOR FILING DATE: 1998-03-13
;; PRIOR APPLICATION NUMBER: 60/078886
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/078936
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/078939
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;; PRIOR APPLICATION NUMBER: 60/079294
;; PRIOR FILING DATE: 1998-03-25
;; PRIOR APPLICATION NUMBER: 60/079556
;; PRIOR FILING DATE: 1998-03-26
;; PRIOR APPLICATION NUMBER: 60/079564
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;; PRIOR FILING DATE: 1998-04-01
;; PRIOR APPLICATION NUMBER: 60/081070
;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/081049
;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/081071

;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/081195
;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/081203
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;; PRIOR APPLICATION NUMBER: 60/084643
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;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 153; DB 10; Length 277;

Best Local Similarity 100.0%; Pred. No. 2e-16; Mismatches 0; Indels 0; Gaps 0;

2y 1 CDCGVRKRVQQLDISIARLKTSMKFKVN 29
db 119 CDCGVRKRVQQLDISIARLKTSMKFKVN 147

RESULT 14

US-09-978-824-97
; Sequence 97, Application US/09978824
; Publication No. US20030055216A1

GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Baker Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleon
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Kljavit, Ivar J.
;; APPLICANT: Kuo, Sophia S.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2630P1C14
;; CURRENT APPLICATION NUMBER: US/09/978,824
;; CURRENT FILING DATE: 2001-10-17
;; PRIOR APPLICATION NUMBER: 09/918585
;; PRIOR FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: 60/062250

;; PRIOR FILING DATE: 1997-10-17
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;; PRIOR APPLICATION NUMBER: 60/084627
;; PRIOR FILING DATE: 1998-05-07
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;; PRIOR FILING DATE: 1998-05-15
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 153; DB 10; Length 277;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CDGGRYKFKVQGLDISIARLKTSMKFVKV 29
Db 119 CDGGRYKFKVQGLDISIARLKTSMKFVKV 147

RESULT 15

US-09-918-585A-97
; Sequence 97, Application US/09918585A
; Publication No. US20030060406A1

GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Baker Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleon
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Kuo, Sophia S.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James;
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2630F1C1
;; CURRENT APPLICATION NUMBER: US/09/918,585A
;; CURRENT FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/064249
;; PRIOR FILING DATE: 1997-11-03
;; PRIOR APPLICATION NUMBER: 60/065311
;; PRIOR FILING DATE: 1997-11-13
;; PRIOR APPLICATION NUMBER: 60/066364
;; PRIOR FILING DATE: 1997-11-21
;; PRIOR APPLICATION NUMBER: 60/077450
;; PRIOR FILING DATE: 1998-03-10

[illegible][illegible]

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:07:46 ; Search time 7.53745 Seconds
(without alignments)
198.629 Million cell updates/sec

Title: US-09-600-932-2_COPY_119_147

Perfect score: 153

Sequence: 1 CDCGRYKFGQLDISIARLKTSMKFVN 29

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/6C COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/6D COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	34.0	3635	4	US-09-845-583A-2
2	49	32.0	487	1	US-08-469-486-53
3	49	32.0	487	2	US-08-469-486-53
4	49	32.0	492	1	US-08-469-486-2
5	49	32.0	492	2	US-08-469-486-2
6	48	31.4	363	4	US-09-328-352-5961
7	47	30.7	113	4	US-09-134-001C-4973
8	46	30.1	106	4	US-09-107-532A-5116
9	46	30.1	279	3	US-09-318-794A-3
10	46	30.1	279	3	US-09-318-793A-5
11	46	30.1	459	3	US-09-118-319-6
12	46	30.1	459	3	US-09-286-691-2
13	46	30.1	459	3	US-09-687-147-2
14	45	29.4	37	6	5187155-10
15	45	29.4	50	6	5187155-9
16	45	29.4	238	4	US-09-664-595A-15
17	45	29.4	241	1	US-08-330-978-4
18	45	29.4	241	1	US-08-474-042-4
19	45	29.4	241	1	US-08-484-558-4
20	45	29.4	241	1	US-08-774-592-4
21	45	29.4	247	3	US-08-944-483-49
22	45	29.4	254	1	US-08-330-978-3
23	45	29.4	254	1	US-08-474-042-3
24	45	29.4	254	1	US-08-484-558-3
25	45	29.4	254	1	US-08-774-592-3
26	45	29.4	306	1	US-08-330-978-1
27	45	29.4	306	1	US-08-474-042-1

Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 4, Appli
Sequence 27, Appli
Sequence 83, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 5026, Ap
Sequence 19, Appli
Sequence 84, Appli

ALIGNMENTS

RESULT 1

US-09-845-583A-2
; Sequence 2, Application US/09845583A
; Patent No. 6635616
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champiaud, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845,583A
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3635
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-845-583A-2

Query Match 34.0%; Score 52; DB 4; Length 3635;
Best Local Similarity 43.5%; Pred. No. 55;
Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 4 GRYKFGVQLDISIARLKTSMKF 26

DB 2636 GRVRKLIQAQSAASKVKVSMKF 2658

RESULT 2

US-08-469-486-53
; Sequence 53, Application US/08469486
; Patent No. 5739281
; GENERAL INFORMATION:
; APPLICANT: Thoegeersen, Hans Christian
; APPLICANT: Holtet, Thor Las
; APPLICANT: Etzerodt, Michael
; TITLE OF INVENTION: Improved method for the refolding of
; NUMBER OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,486
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/002001
TELEPHONE: 617 542 5070
TELEFAX: 617 542 8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-469-486-53

Query Match 32.0%; Score 49; DB 1; Length 487;
Best Local Similarity 40.0%; Pred. No. 18;
Matches 10; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 5 RYKFGVGLDGIARLKTSMKFKVN 29
DB 312 RFVKETYDFDIARLKTPIRFRN 336

RESULT 3
US-08-469-658-53
Sequence 53, Application US/08469658
Patent No. 5917018
GENERAL INFORMATION:
APPLICANT: Th. egersen, Hans Christian
APPLICANT: Holtet, Thor Las
APPLICANT: Etzerodt, Michael
TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOLDING OF
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,658
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark

REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/002002
TELEPHONE: 617 542 5070
TELEFAX: 617 542 8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-469-658-53

Query Match 32.0%; Score 49; DB 2; Length 487;
Best Local Similarity 40.0%; Pred. No. 18;
Matches 10; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 5 RYKFGVGLDGIARLKTSMKFKVN 29
DB 312 RFVKETYDFDIARLKTPIRFRN 336

RESULT 4
US-08-469-486-2
Sequence 2, Application US/08469486
Patent No. 5739281
GENERAL INFORMATION:
APPLICANT: Thøgersen, Hans Christian
APPLICANT: Holtet, Thor Las
APPLICANT: Etzerodt, Michael
TITLE OF INVENTION: Improved method for the refolding of
TITLE OF INVENTION: proteins
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,486
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/002001
TELEPHONE: 617 542 5070
TELEFAX: 617 542 8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-469-486-2

Query Match 32.0%; Score 49; DB 1; Length 492;


```

Best Local Similarity 40.0%; Pred No. 18;
Matches 10; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

2Y 5 RYKRVGQGLDISIARLKTSMKFVKV 29
   | | | | | | | | | | | | | |
3b 312 RFVKETYDFDI AVLRLKTPIRFRN 336

RESULT 5
JS-08-469-658-2
; Sequence 2, Application US/08469658
; Patent No. 5917018
; GENERAL INFORMATION:
; APPLICANT: Th egersen, Hans Christian
; APPLICANT: Holtet, Thor Las
; APPLICANT: Etzerodt, Michael
; TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOOLDING OF
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version
; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,658
; FILING DATE: June 5, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/192,060
; FILING DATE: February 4, 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06363/002002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 542 5070
; TELEFAX: 617 542 8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 492 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
JS-08-469-658-2

Query Match 32.0%; Score 49; DB 2; Length 492;
Best Local Similarity 40.0%; Pred No. 18;
Matches 10; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

2Y 5 RYKRVGQGLDISIARLKTSMKFVKV 29
   | | | | | | | | | | | | | |
3b 312 RFVKETYDFDI AVLRLKTPIRFRN 336

RESULT 6
US-09-328-352-5961
; Sequence 5961, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

```

APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariadello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5116:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...106
SEQUENCE DESCRIPTION: SEQ ID NO: 5116:
US-09-107-532A-5116

Query Match 30.1%; Score 46; DB 4; Length 106;
Best Local Similarity 30.8%; Pred. No. 9.6;
Matches 8; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 4 GRYKFKVQGLDISIARLK 29
DB 70 GTIRKVSQGLPKIDTIVRFKKS 95

RESULT 9
US-09-318-794A-3
Sequence 3, Application US/09318794A
Patent No. 6177264
GENERAL INFORMATION:
APPLICANT: DEGUSSA AKTIENGESCHLAF
TITLE OF INVENTION: METHOD FOR THE FERMENTATIVE PRODUCTION OF D-PANTOTHENIC
TITLE OF INVENTION: ACID USING CORNEFORM BACTERIA
FILE REFERENCE: eggeling
CURRENT APPLICATION NUMBER: US/09/318,794A
CURRENT FILING DATE: 1999-05-26
PRIOR APPLICATION NUMBER: DE 198 55 312.9
PRIOR FILING DATE: 1998-12-01
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 279
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-318-794A-3

Query Match 30.1%; Score 46; DB 3; Length 279;
Best Local Similarity 45.0%; Pred. No. 28;
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 DCGRYKFKVQGLDISIARLK 21
DB 63 DCDYRNYPRQLDADLALLE 82

RESULT 10
US-09-318-793A-5
Sequence 5, Application US/09318793A
Patent No. 6184007
GENERAL INFORMATION:

APPLICANT: Dusch, Nicole
APPLICANT: Kalinowski, Jorn
APPLICANT: Puhler, Alfred
TITLE OF INVENTION: METHOD FOR THE FERMENTATIVE PRODUCTION OF D-PANTOTHENIC
TITLE OF INVENTION: ACID BY ENHANCEMENT OF THE pand GENE IN MICROORGANISMS
FILE REFERENCE: 21123/260204
CURRENT APPLICATION NUMBER: US/09/318,793A
CURRENT FILING DATE: 1999-05-26
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 279
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-318-793A-5

Query Match 30.1%; Score 46; DB 3; Length 279;
Best Local Similarity 45.0%; Pred. No. 28;
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 DCGRYKFKVQGLDISIARLK 21
DB 63 DCDYRNYPRQLDADLALLE 82

RESULT 11
US-09-118-319-6
Sequence 6, Application US/09118319
Patent No. 6114158
GENERAL INFORMATION:
APPLICANT: Li, Xin-liang
APPLICANT: Chen, Huizhong
APPLICANT: Ljungdahl, Lars G.
TITLE OF INVENTION: Orpinomyces Cellulase Celf Protein and Coding Sequences
FILE REFERENCE: 33-98sequence listing
CURRENT APPLICATION NUMBER: US/09/118,319
CURRENT FILING DATE: 1998-07-17
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 459
TYPE: PRT
ORGANISM: Orpinomyces sp. PC-2
US-09-118-319-6

Query Match 30.1%; Score 46; DB 3; Length 459;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 8 KFGVQGLDISIARLKSMK 25
DB 143 KFGVEVDISIKKLGDLK 160

RESULT 12
US-09-286-691-2
Sequence 2, Application US/09286691
Patent No. 6190189
GENERAL INFORMATION:
APPLICANT: Li, Xin-Liang
APPLICANT: Ljungdahl, Lars G.
APPLICANT: Chen, Huizhong
TITLE OF INVENTION: Cellulases and Coding Sequences
FILE REFERENCE: 42-96
CURRENT APPLICATION NUMBER: US/09/286,691
CURRENT FILING DATE: 1999-04-05
EARLIER APPLICATION NUMBER: US 60/027,883
EARLIER FILING DATE: 1996-10-04
EARLIER APPLICATION NUMBER: PCT US97/18008
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2

/ LENGTH: 459
/ TYPE: PRT
/ ORGANISM: Orpinomyces sp. PC-2
US-09-286-691-2

Query Match 30.1%; Score 46; DB 3; Length 459;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 8 KFGVGLDISIARLKTSMK 25
DB 143 KPQGEVDISIKKNGDLK 160

RESULT 13

US-09-687-147-2

/ Sequence 2; Application US/09687147

/ Patent No. 6268198

/ GENERAL INFORMATION:

/ APPLICANT: Li, Xin-Liang

/ APPLICANT: Ljungdahl, Lars G.

/ APPLICANT: Chen, Huizhong

/ TITLE OF INVENTION: Cellulases and Coding Sequences

/ FILE REFERENCE: 42-96a

/ CURRENT APPLICATION NUMBER: US/09/687,147

/ PRIOR FILING DATE: 2000-10-12

/ PRIOR APPLICATION NUMBER: US 60/027,883

/ PRIOR FILING DATE: 1996-10-04

/ PRIOR APPLICATION NUMBER: PCT US97/18008

/ PRIOR FILING DATE: 1997-10-03

/ PRIOR APPLICATION NUMBER: 09/286,691

/ PRIOR FILING DATE: 1999-04-05

/ NUMBER OF SEQ ID NOS: 29

/ SOFTWARE: PatentIn Ver. 2.0

/ SEQ ID NO 2

/ LENGTH: 459

/ TYPE: PRT

/ ORGANISM: Orpinomyces sp. PC-2

US-09-687-147-2

Query Match

Best Local Similarity 30.1%; Score 46; DB 3; Length 459;

Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 8 KFGVGLDISIARLKTSMK 25
DB 143 KPQGEVDISIKKNGDLK 160

RESULT 14

5187155-10

/ Patent No. 5187155

/ APPLICANT: FAIR, DARYL S.

/ TITLE OF INVENTION: ANTICOAGULANT PEPTIDES

/ NUMBER OF SEQUENCES: 27

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/07/371,561

/ FILING DATE: 23-JUN-1989

/ SEQ ID NO:10:

/ LENGTH: 37

5187155-10

Query Match

Best Local Similarity 29.4%; Score 45; DB 6; Length 37;

Matches 10; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 5 RYRKFGVGLDISIARLKTSMKFKVN 29
DB 7 RPTKETDYDFDI AVLRLKPTPTFRMN 31

RESULT 15

5187155-9

/ Patent No. 5187155
/ APPLICANT: FAIR, DARYL S.
/ TITLE OF INVENTION: ANTICOAGULANT PEPTIDES
/ NUMBER OF SEQUENCES: 27
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/371,561
/ FILING DATE: 23-JUN-1989
/ SEQ ID NO:9:
/ LENGTH: 50
5187155-9

Query Match 29.4%; Score 45; DB 6; Length 50;

Best Local Similarity 40.0%; Pred. No. 6;

Matches 10; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 5 RYRKFGVGLDISIARLKTSMKFKVN 29
DB 20 RPTKETDYDFDI AVLRLKPTPTFRMN 44

Search completed: March 8, 2004, 12:17:28

Job time : 8.53745 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 11:54:00 ; Search time 26.7004 Seconds
(without alignments)

Title: US-09-600-932-2 COPY 119 147

Perfect score: 153
Sequence: 1 CDCGRYRKFGQLDISIARLKTSMKFVQN 29

Scoring table: BLOSUM62

Searched: 1586107 segs. 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneset 29Jan04:*

1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003ae.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	153	100.0	159	5	ABb56404	Human col
2	153	100.0	277	2	AAy25518	Human ccl
3	153	100.0	277	2	AAy41698	Human PRO
4	153	100.0	277	3	AAb44254	Human PRO
5	153	100.0	277	4	AAU29073	Human PRO
6	153	100.0	277	6	ABu58449	Human PRO
7	153	100.0	277	6	ABU87997	Novel hum
8	153	100.0	277	6	ABU84312	Human sec
9	153	100.0	277	6	ABR66186	Human sec
10	153	100.0	277	6	ABR65576	Human sec
11	153	100.0	277	6	ABU99516	Human sec
12	153	100.0	277	6	ABU82755	Human PRO
13	153	100.0	277	6	ABU98876	Novel hum
14	153	100.0	277	6	ABR68125	Human sec
15	153	100.0	277	6	ABU96178	Novel hum
16	153	100.0	277	6	ABU92609	Human sec
17	153	100.0	277	6	ABO08686	Human sec
18	153	100.0	277	6	ABO02738	Human sec
19	153	100.0	277	6	ABr74892	Human sec
20	153	100.0	277	6	ABr94654	Human sec
21	153	100.0	277	6	ABO45200	Novel hum
22	153	100.0	277	6	ABU85627	Human PRO
23	153	100.0	277	6	ABU98787	Novel hum
24	153	100.0	277	6	ABU98002	Novel hum
25	153	100.0	277	6	ABU91708	Novel hum

Sequence 159 AA:

Query Match 100.0% Score 153: DB 5: Length 159:

Query Match	100.0%;	Score 133;	DB 31
Best Local Similarity	100.0%;	Pred. No. 1.1e-15;	

ALIGNMENTS

RESULT 1

ABB56404
ID ABB56404 standard; peptide; 159 AA.

AC ABB56404:

XX
DT 19-FEB-2002 (first entry)

Human collectin polypeptide SEO ID NO 52.

XX Human; collectin; CL-L2-1; CL-L2-2; mouse; antibacterial; virucide;
KW
KW protein therapy; infection; ds.

XX
OS
Homo sapiens

XX
PN
WC200181401-A1XX
PD
01-NOV-2001

XX
DE
23-APR-2001.

XX
PB 31-APB-3000-3000TB-00130358

XX
PA
XX

XX
DT Wakemura N Yochi u Ohts

XX
DB WDT. 2002-0624E/A7

XX
New collection family
DE

PT in kidney and for treatment and prevention of bacterial and viral infections

2000

100

CC L2-2, sequences given in the specification, ABB56407-ABB56411 and
CC ABB56414-ABB56416), their derivatives and fragments and a related
CC collectin (CL-L2) of mouse origin (ABB56412) and polynucleotides encoding
CC all or part of the proteins. The proteins have antibacterial and virucide
CC activity and are used for protein therapy and treatment, prevention and
CC diagnosis of bacterial and viral infections. The present sequence is that
CC of a collectin polynucleotide of the invention

Sequence 159 AA:

Query Match 100.0% Score 153: DB 5: Length 159:

Query Match	100.0%;	Score 133;	DB 31
Best Local Similarity	100.0%;	Pred. No. 1.1e-15;	

```
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CDCGRRKRVGQDLSIARLKTSMKFKVN 29
DB 1 CDCGRRKRVGQDLSIARLKTSMKFKVN 29

RESULT 2
AA425518
ID AA425518 standard; protein; 277 AA.
XX AC AA425518;
XX DT 30-SEP-1999 (first entry)
XX DE Human collectin protein.
XX KW Collectin; human; antibacterial; antiviral; treatment; infection.
XX OS Homo sapiens.
XX PN WO9937767-A1.
XX PD 29-JUL-1999.
XX PF 24-JUL-1998; 98WO-JP003328.
XX PR 23-JAN-1998; 98JP-00011281.
XX PA (FUSO) FUSO PHARM IND LTD.
XX PI Wakamiya N;
XX DR WPI; 1999-458691/38.
XX DR N-PSDB; AA488323.
XX PT New collectin protein of human origin and DNA encoding it.
XX PS Claim 1; Page 42-44; 58pp; Japanese.
XX CC This invention describes the isolation and characterization of a novel
CC human collectin protein and its encoding polynucleotide. The human
CC collectin exhibits antibacterial and antiviral activity and can be used
CC as an agent for the treatment of human bacterial and viral infections.
CC This sequence represents the novel human collectin
XX SQ Sequence 277 AA;

Query Match 100.0%; Score 153; DB 2; Length 277;
Best Local Similarity 100.0%; Pred. No. 2e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CDCGRRKRVGQDLSIARLKTSMKFKVN 29
DB 119 CDCGRRKRVGQDLSIARLKTSMKFKVN 147

RESULT 3
AA41698
ID AA41698 standard; protein; 277 AA.
XX AC AA41698;
XX DT 07-DEC-1999 (first entry)
XX DE Human PRO702 protein sequence.
XX KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
XX probe; blood coagulation disorder; cancer; cellular adhesion disorder;
XX secreted protein; transmembrane protein.
XX OS Homo sapiens.
XX PN WO9946281-A2.
XX PD 16-SEP-1999.
XX PE 08-MAR-1999; 99WO-US005028.
XX PR 10-MAR-1998; 98US-0077450P.
XX PR 11-MAR-1998; 98US-0077632P.
XX PR 11-MAR-1998; 98US-0077641P.
XX PR 12-MAR-1998; 98US-0077649P.
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XX
PA (GETH ) GENENTECH INC.
XX
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
DR WPI: 1999-551358/46.
XX N-PSDB; AAZ333973.
XX
PT New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders.
XX
PS Claim 12; Fig 37; 530pp; English.
XX
CC The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as sources
CC of probes, primers, for chromosome mapping, and for generation of
CC antisense sequences. They can also be used to create transgenic animals.
CC The proteins can be used to treat a variety of diseases and disorders,
CC depending on their function. Diseases that may be treated include blood
CC coagulation disorders, cancers and cellular adhesion disorders. They may
CC also be used to raise antibodies. AAZ33391 to AAZ4338, and AAZ41685 to
CC AAZ41774 represent polynucleotide and polypeptide sequences given in the
CC exemplification of the present invention
XX
SQ Sequence 277 AA;
XX
Query Match 100.0%; Score 153; DB 2; Length 277;
Best Local Similarity 100.0%; Pred. NO. 2e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CDCGRRKRVGQLDISIARLKTSMKFVK 29
DB 119 CDCGRRKRVGQLDISIARLKTSMKFVK 147
RESULT 4
AAB44254
ID AAB44254 standard; protein; 277 AA.
XX
AC AAB44254;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human PRO702 (UNQ366) protein sequence SEQ ID NO:97.
XX
KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
KW expressed sequence tag; detection; cancer.
XX
OS Homo sapiens.
XX
PN WO200053756-A2.

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XX
PD 14-SEP-2000.
XX
PF 18-FEB-2000; 2000WO-US004341.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
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PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Deenoyers L, Baton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Kljavin LJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI: 2000-611443/58.
DR N-PSDB; AAC78480.
XX
PT Novel PRO polypeptides and polynucleotides used in detection methods, to
PT target bioactive molecules to specific cells, and to modulate cellular
PT activities.
XX
PS Claim 12; Fig 37; 636pp; English.
XX
CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
CC tag) sequences which encode secreted or transmembrane PRO polypeptides.
CC The PRO polynucleotides and polypeptides have cytostatic activity. The
CC polynucleotides and polypeptides can be used for detecting the presence
CC of PRO polypeptides in samples, for linking bioactive molecules to cells
CC and for modulating biological activities of cells, using the polypeptides
CC for specific targeting. The polypeptide targeting can be used to kill the
CC target cells, e.g. for the treatment of cancers. The polypeptide pairs
CC provide specific targeting of bioactive molecules to cells. AAC78600 to
CC AAC78987 represent PCR primers and probes used in the isolation of the
CC PRO polynucleotide sequences
XX
SQ Sequence 277 AA;
XX
Query Match 100.0%; Score 153; DB 3; Length 277;
Best Local Similarity 100.0%; Pred. NO. 2e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CDCGRRKRVGQLDISIARLKTSMKFVK 29
DB 119 CDCGRRKRVGQLDISIARLKTSMKFVK 147
RESULT 5
AAU29073
ID AAU29073 standard; protein; 277 AA.
XX
AC AAU29073;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human PRO polypeptide sequence #50.

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XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
DS Homo sapiens.
XX WO200168848-A2.
XX
XX 20-SEP-2001.
XX
XX 28-FEB-2001; 2001WO-US006520.
XX
XX 01-MAR-2000; 2000WO-US005601.
XX 02-MAR-2000; 2000WO-US005841.
XX 03-MAR-2000; 2000US-0187202P.
XX 06-MAR-2000; 2000US-0186986P.
XX 14-MAR-2000; 2000US-0189320P.
XX 14-MAR-2000; 2000US-0189328P.
XX 15-MAR-2000; 2000WO-US006884.
XX 21-MAR-2000; 2000US-0190828P.
XX 21-MAR-2000; 2000US-0191007P.
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XX 30-MAR-2000; 2000WO-US008439.
XX 04-APR-2000; 2000US-0194449P.
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XX 25-APR-2000; 2000US-0199397P.
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XX 25-APR-2000; 2000US-0199654P.
XX 03-MAY-2000; 2000US-0201516P.
XX 17-MAY-2000; 2000WO-US013705.
XX 22-MAY-2000; 2000WO-US014042.
XX 30-MAY-2000; 2000WO-US014941.
XX 02-JUN-2000; 2000WO-US015264.
XX 05-JUN-2000; 2000US-0209832P.
XX 28-JUL-2000; 2000WO-US020710.
XX 22-AUG-2000; 2000US-00644848.
XX 24-AUG-2000; 2000WO-US023328.
XX 08-NOV-2000; 2000WO-US030952.
XX 01-DEC-2000; 2000WO-US032578.
XX 20-DEC-2000; 2000WO-US034956.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
XX Pan J, Smith V, Watanabe CK, Wood WJ, Zhang Z;
XX
XX WPI: 2001-602746/68.
XX N-PSDB; AAS45974.
XX
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
XX presence of tumors, such as prostate and breast tumors, in mammals and to
XX screen for modulators of the compounds.
XX
XX Claim 11; Fig 100; 774pp; English.
XX
XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
XX The PRO polypeptides and their associated nucleic acids can be used to
XX detect the presence of a tumour in a mammal by comparing the level of
XX expression of a PRO polypeptide in a test sample of cells from the animal
XX and a control sample of normal cells, whereby a higher level of

CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders
XX
XX Sequence 277 AA;

Query Match 100.0%; Score 153; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 2e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDGGRYKFKVQGLDISIARLKTSMKFVKV 29
Db 119 CDGGRYKFKVQGLDISIARLKTSMKFVKV 147

RESULT 6

ABUS8449
ID ABUS8449 standard; protein; 277 AA.

XX AC ABUS8449;

XX 15-APR-2003 (first entry)

XX Human PRO polypeptide #50.

XX Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
XX dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
XX antibody-dependent enzyme mediated prodrug therapy.

XX Homo sapiens.

XX US2003027272-A1.

XX 06-FEB-2003.

XX 21-JUN-2002; 2002US-00176492.

XX 18-SEP-1997; 97US-0059263P.

XX 18-SEP-1997; 97US-0059266P.

XX 17-OCT-1997; 97US-0062505P.

XX 21-OCT-1997; 97US-0063486P.

XX 24-OCT-1997; 97US-0063120P.

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XX 28-OCT-1997; 97US-0063544P.

XX 28-OCT-1997; 97US-0063564P.

XX 29-OCT-1997; 97US-0063734P.

XX 31-OCT-1997; 97US-0063870P.

XX 31-OCT-1997; 97US-0064103P.

XX 13-NOV-1997; 97US-0065311P.

XX 21-NOV-1997; 97US-0066120P.

XX 24-NOV-1997; 97US-0066466P.

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XX 10-MAR-1998; 98US-0077450P.

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KW tissue typing.
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XX DT 05-AUG-2003 (first entry)
XX DE Human secreted polypeptide PRO702, SEQ ID NO:100.
XX KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnary; gene therapy.
XX OS Homo sapiens.
XX PN US2003027278-A1.
XX PD 06-FEB-2003.
XX PF 21-JUN-2002; 2002US-00176987.
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Query Match 100.0%; Score 153; DB 6; Length 277;
Best Local Similarity 100.0%; Pred. No. 2e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDGGRYKRVGQIDSIARLKTSMKPVKN 29
Db 119 CDGGRYKRVGQIDSIARLKTSMKPVKN 147

RESULT 10
ABR65576
ID ABR65576 standard; protein; 277 AA.
XX
AC ABR65576;

XX 05-AUG-2003 (first entry)
DT Human secreted polypeptide PRO702, SEQ ID NO:100.
XX
DE Human; PRO; secreted protein; transmembrane protein;
XX extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnery; gene therapy.
XX Homo sapiens.
OS
XX US2003036159-A1.
PN
XX 20-FEB-2003.
PD
XX 02-JUL-2002; 2002US-00188773.
PF
XX 18-SEP-1997; 97US-0059263P.
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XX OS Homo sapiens.
XX PN US2003040070-A1.
XX XX
PD 27-FEB-2003.
XX PF
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Query Match 100.0%; Score 153; DB 6; Length 277;
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Qy 1 CDCGRYKRVGQLDISIARLKTSMKPFVN 29
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 Db 119 CDCGRYKRVGQLDISIARLKTSMKPFVN 147
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RESULT 13

ABU89876
 ID ABU89876 standard; protein; 277 AA.

XX AC ABU89876;

XX 11-AUG-2003 (first entry)

XX DE Novel human secreted and transmembrane protein PRO702.

XX Human; gene therapy; tissue typing; tumour; chondrocyte proliferation;
 XX chondrocyte differentiation; tumour necrosis factor-alpha release;
 XX affinity purification.

XX OS Homo sapiens.

XX PN US2003036147-A1.

XX PD 20-FEB-2003.

XX PF 02-JUL-2002; 2002US-00187741.

XX PR 18-SEP-1997; 97US-0059263P.

XX PR 18-SEP-1997; 97US-0059266P.

XX PR 17-OCT-1997; 97US-0062250P.

XX PR 21-OCT-1997; 97US-0063486P.


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Query Match 100.0%; Score 153; DB 6; Length 277;
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Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 119 CDGGRYKRVQQLDISARLKTSMKFKVN 147

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ASR68125
ID ABR68125 standard; protein; 277 AA.
XX AC ABR68125;
XX DT 11-AUG-2003 (first entry)
XX DE Human secreted polypeptide PRO702, SEQ ID NO:100.
XX KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnary; gene therapy.
XX OS Homo sapiens.
XX PN US2003027264-A1.
XX PD 06-FEB-2003.
XX PP 18-JUN-2002; 2002US-00174579.
XX PR 18-SEP-1997; 97US-0059263P.
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PR 06-MAY-1998; 98US-0084414P.
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PR 15-MAY-1998; 98US-0085580P.
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PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.

Query Match 100.0%; Score 153; DB 6; Length 277;

Best Local Similarity 100.0%; Pred. No. 2e-15;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCGRYKFGQDISIARLKTSMKFVN 29

Db 119 CDCGRYKFGQDISIARLKTSMKFVN 147

RESULT 15

ID ABU96178 standard; protein; 277 AA.

XX AC ABU96178;

XX DT 25-JUL-2003 (first entry)

XX DE Novel human secreted and transmembrane protein PRO702.

XX KW Human; secreted and transmembrane protein; PRO; transgenic animal;
XX KW knockout; chromosome identification; tissue typing; tumour;
XX KW chondrocyte proliferation; chondrocyte differentiation;
XX KW tumor necrosis factor-alpha release stimulator.

XX OS Homo sapiens.

XX XX US2003036144-A1.

XX XX 20-FEB-2003.

XX XX 01-JUL-2002; 2002US-00187601.

XX PR 18-SEP-1997; 97US-0059263P.

XX PR 18-SEP-1997; 97US-0059266P.

XX PR 17-OCT-1997; 97US-0062250P.

XX PR 21-OCT-1997; 97US-0063486P.

XX PR 24-OCT-1997; 97US-0063120P.

XX PR 24-OCT-1997; 97US-0063121P.

XX PR 28-OCT-1997; 97US-0063540P.

XX PR 28-OCT-1997; 97US-0063541P.

XX PR 28-OCT-1997; 97US-0063544P.

XX PR 29-OCT-1997; 97US-0063734P.

XX PR 31-OCT-1997; 97US-0063870P.

XX PR 31-OCT-1997; 97US-0064103P.

XX PR 13-NOV-1997; 97US-0065311P.

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XX PR 24-NOV-1997; 97US-0066466P.

XX PR 24-NOV-1997; 97US-0066772P.


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PR 29-SEP-1998; 98US-0102331P.
PR 29-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
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PR 06-OCT-1998; 98US-0103449P.

Query Match 100.0%; Score 153; DB 6; Length 277;
Best Local Similarity 100.0%; Pred. No. 2e-15;
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2y 1 CDCGRYKFKVCGQLDISIARLKTSMKFKVN 29
db 119 CDCGRYKFKVCGQLDISIARLKTSMKFKVN 147
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Search completed: March 8, 2004, 12:11:23
Job time : 27.7004 secs

GenCore version 5.1.6
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DM protein - protein search, using sw model

Run on: March 8, 2004, 12:03:01 ; Search time 7.652 Seconds
(without alignments)
363.925 Million cell updates/sec

Title: US-09-600-932-2_COPY_119_147

Perfect score: 153

Sequence: 1 CDCGRYKFKVQGLDISIARLKTSMKFKVN 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*
1: Pirl.*
2: Pirl2.*
3: Pirl3.*
4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	144	94.1	277	JC7903	collectin liver 1
2	52	34.0	3635	T10053	laminin alpha 5 ch
3	49	32.0	188	T40222	hypothetical prote
4	49	32.0	492	EXBO	coagulation factor
5	49	32.0	964	D59404	plectin isoform pl
6	49	32.0	1239	A45648	DNA topoisomerase
7	49	32.0	4574	G02520	plectin - human
8	49	32.0	4684	A59404	plectin (imported)
9	49	32.0	4687	A39638	plectin - rat
10	48	31.4	265	G96931	homocitrate syntha
11	48	31.4	465	A82211	Mut/nudix family
12	48	31.4	607	A95122	Tn5252 relaxase [
13	47.5	31.0	358	G56998	hypothetical prote
14	47	30.7	191	AH1571	alpha-ribazole-5'-
15	47	30.7	265	C90026	hypothetical prote
16	47	30.7	283	T50431	CBP3-like protein
17	46.5	30.4	581	P84599	probable kinesin h
18	46	30.1	279	T47120	pantoate-beta-alan
19	46	30.1	400	JC2473	dcc2 protein - hum
20	46	30.1	447	A86647	hypothetical prote
21	46	30.1	491	T23527	hypothetical prote
22	46	30.1	508	A72201	UDP-sugar diphosph
23	46	30.1	604	S57065	probable membrane
24	45.5	29.7	167	F64314	methyl coenzyme M
25	45.5	29.7	1295	T21720	hypothetical prote
26	45	29.4	127	A21989	steroid delta-5-3-
27	45	29.4	279	G37246	araC-type DNA-bind
28	45	29.4	283	F95893	probable ABC trans
29	45	29.4	341	F90321	glycosyltransferase

ALIGNMENTS

RESULT 1

JC7903
collectin liver 1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-2003 #sequence_revision 03-Feb-2003 #text_change 31-Mar-2003
C:Accession: JC7903
R:Kawai, T.; Suzuki, Y.; Eda, S.; Kase, T.; Ohtani, K.; Sakai, Y.; Keshi, H.; Fukuchi, A
Biosci. Biotechnol. Biochem. 66, 2134-2145, 2002
A:Title: Molecular cloning of mouse collectin liver 1.
A:Reference number: JC7903; MUID:22333927; PMID:12450124
A:Accession: JC7903
A:Molecule type: mRNA
A:Residues: 1-277 <RAW>
A:Cross-references: DDBJ:AB016429
A:Experimental source: liver
C:Comment: This protein is a highly conserved cytosolic protein and belongs to a vertebr
c development.
C:Genetics:
A:Gene: Cl11
A:Map position: 15

Query Match 94.1%; Score 144; DB 2; Length 277;
Best Local Similarity 89.7%; Pred. No. 2.5e-14;
Matches 26; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CDCGRYKFKVQGLDISIARLKTSMKFKVN 29

Db 119 CDCGRYKFKVQGLDISIARLKTSMKFKVN 147

RESULT 2

T10053
laminin alpha 5 chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2003
C:Accession: T10053
R:Miner, J.H.; Lewis, R.M.; Sanes, J.R.
submitted to the EMBL Data Library, November 1997
A:Reference number: Z16923
A:Accession: T10053
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-3635 <MIN>
A:Cross-references: EMBL:U37501; NID:G2599231; PID:G2599232
C:Genetics:
A:Gene: Lama5
C:Keywords: basement membrane; cell binding; extracellular matrix
F:1888-1939/Domain: laminin-type EGF-like homology <LEG>
F:1942-1970/Domain: EGF homology <EGF>

Query Match 34.0%; Score 52; DB 2; Length 3635;
Best Local Similarity 43.5%; Pred. No. 43;

Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 4 GRYKRVGQLDISIRLKTSMKF 26
| | | | : : : | | |
Db 2636 GRVREKLIQAARSAASAKVKVSMKF 2658

RESULT 3
I40222
Hypochemical protein 4 - Bacillus licheniformis (fragment)
C:Species: Bacillus licheniformis
C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Oct-1999
C:Accession: I40222
R:Harry, E.J.; Partridge, S.R.; Weiss, A.S.; Wake, R.G.
Gene 147, 85-89, 1994
A>Title: Conservation of the 168 divIB gene in Bacillus subtilis W23 and B. licheniformis
A:Reference number: I40220; MUID:94374713; PMID:8088553
A:Accession: I40222
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-188 <REG>
A:Cross-references: EMBL:U01958; NID:9404008; PIDN:AAA57245.1; PID:G602399
C:Genetics:
A:Start codon: TTG

Query Match 32.0%; Score 49; DB 2; Length 188;
Best Local Similarity 37.5%; Pred. No. 6.5;
Matches 9; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 2 DCGRYKRVGQLDISIRLKTSMK 25
| | | | | : : : | : : |
Db 90 DVERYMFVGEIGVQGEIKRITLK 113

RESULT 4
EXPO
coagulation factor Xa (EC 3.4.21.6) precursor - bovine
N:Alternate names: Stuart factor
C:Species: Bos primigenius taurus (cattle)
C>Date: 24-Apr-1984 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
C:Accession: A22867; A14997; A12030; A34412; S39414; A00925
R:Fung, M.R.; Campbell, R.M.; MacGillivray, T.A.
Nucleic Acids Res. 12, 4481-4492, 1984
A>Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a
A:Reference number: A22867; MUID:84247315; PMID:6330671
A:Accession: A22867
A:Molecule type: mRNA
A:Residues: 1-487 <FUN>
A:Cross-references: GB:X00673; NID:G192; PIDN:CAA25286.1; PID:G193
R:Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.
Biochemistry 19, 659-667, 1980
A>Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).
A:Reference number: A14997; MUID:80130563; PMID:6766735
A:Accession: A14997
A:Molecule type: protein
A:Residues: 41-102, N', 104-180 <ENF>
R:McMullen, B.A.; Fujikawa, K.; Kisilev, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A>Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
A:Reference number: A20274; MUID:83308813; PMID:6688526
A:Contents: annotation; revision to residue 103
R:Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.
Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975
A>Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.
A:Reference number: A12030; MUID:76053069; PMID:1059093
A:Accession: A12030
A:Molecule type: protein
A:Residues: 183-292,294-295, GDE', 299-334, 336-349, 'AE', 351-354,356-441, 'GRKG', 446-492 <T
A>Note: carboxylate binding sites and disulfide bonds were determined
R:Ericsson, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oellin, A.K.; Stenflo, J.
J. Biol. Chem. 264, 16897-16904, 1989
A>Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal
A:Reference number: A34412; MUID:89380326; PMID:2789221

A:Accession: A34412
A:Molecule type: protein
A:Residues: 85-126 <PER>
A>Note: beta-hydroxyaspartic acid site
R:Inoue, K.; Morita, T.
Eur. J. Biochem. 218, 153-163, 1993
A>Title: Identification of O-linked oligosaccharide chains in the activation peptides of
A:Reference number: S39414; MUID:94062825; PMID:8243461
A:Accession: S39414
A:Molecule type: protein
A:Residues: 183-196,199-209;216-233 <INO>
A>Note: carboxylate binding sites
R:Titani, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; I
Biochemistry 11, 4899-4903, 1972
A>Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mammali
A:Reference number: A12453; MUID:73053314; PMID:4264286
A:Contents: annotation; active site
R:Fujikawa, K.; Titani, K.; Davies, E.W.
Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975
A>Title: Activation of bovine factor X (Stuart factor): conversion of factor Xaalpha to
A:Reference number: A13504; MUID:76053121; PMID:1059122
A:Contents: annotation; activation
R:Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.
J. Biol. Chem. 259, 5705-5710, 1984
A>Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic
A:Reference number: A38024; MUID:84185716; PMID:6546930
A:Contents: annotation; calcium binding
R:Morita, T.; Jackson, C.M.
J. Biol. Chem. 261, 4008-4014, 1986
A:Reference number: A38025; MUID:86140210; PMID:3949800
A:Contents: annotation; sulfate binding
A:Comment: Factor Xa converts prothrombin to thrombin during blood clotting.
C:Comment: The two chains are formed from a single-chain precursor by the excision of tv
C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), c
activation.
C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strc
C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamir
A:Gene: F10
A:Map position: 13q34
C:Function:
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutan
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-40/Domain: propeptide #status predicted <PRO>
F:41-180/Domain: Gla domain homology <GLA>
F:41-180/Product: coagulation factor X light chain #status experimental <LCH>
F:129-164/Domain: EGF homology <EGF>
F:183-233/Domain: coagulation peptide #status experimental <APT>
F:234-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>
F:234-461/Domain: trypsin homology <TRY>
F:46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #s
F:57-62,90-101,95-110,112-129,140,136-149,151-164,172-341/disulfide bonds: #status i
F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:200/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
F:208,485/Binding site: carboxylate (Thr) (covalent) #status experimental
F:218/Binding site: carboxylate (Asn) (covalent) #status experimental
F:233-234/Cleavage site: Arg-11e (coagulation factor IXa, coagulation factor VIIa) #stat
F:240-245,260-278,389-403,414-442/Disulfide bonds: #status experimental
F:275,321,418/Active site: His, Asp, Ser #status predicted

Query Match 32.0%; Score 49; DB 1; Length 492;
Best Local Similarity 40.0%; Pred. No. 17;
Matches 10; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 5 RYRKEVQQLDISIRLKTSMKFVKN 29
| | | | | : : : | : : |
Db 312 RYRKEVQQLDISIRLKTSMKFVKN 336


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>Query Match
>Best Local Similarity 32.0%; Score 49; DB 2; Length 964;
>Species: Mus musculus (house mouse)
>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
>Accession: D59404
>Fuchs, P.; Zorer, M.; Reznicek, G.A.; Spazierer, D.; Oehler, S.; Castanon, M.J.; Hauptmann, M.; Genet, S.; 2461-2472, 1999
>Title: Unusual 5' transcript complexity of plectin isoforms: novel tissue-specific exc
>Reference number: D59404; MUID:20025755; PMID:10556294
>Accession: D59404
>Status: preliminary
>Molecule type: DNA
>Residues: 1-964 <STO>
>Cross-references: GB:AAF18069; NID:G6578735; PIDN:AAF18065.1

Query Match 32.0%; Score 49; DB 2; Length 964;
Best Local Similarity 45.5%; Pred. No. 33;
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

> 4 GRYKFKVQGLDISIARLKTSMK 25
> 733 GAYRDCGLGRDLQYAKLLNSSK 754

>RESULT 6
>NA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3), kinetoplast-associated - Crithidia fa
>Alternate names: type II DNA topoisomerase
>Species: Crithidia fasciculata
>Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
>Accession: A45648; S15456
>Pasion, S.G.; Hines, J.C.; Lebersold, R.; Ray, D.S.
>Title: Molecular cloning and expression of the gene encoding the kinetoplast-associated
>Reference number: A45648; MUID:92178291; PMID:1311798
>Accession: A45648
>Molecule type: DNA; protein
>Residues: 1-1239 <PAS>
>Cross-references: EMBL:X59623; NID:g11000; PIDN:CAA42182.1; PID:g11001
>Note: sequence extracted from NCBI backbone (NCBI:85204)
>Comment: The same gene may encode the nuclear and kinetoplast (mitochondrial) forms of
>Superfamily: eukaryotic type II DNA topoisomerase; phage T4 DNA topoisomerase (ATP-hyd
>Keywords: DNA binding; isomerase; mitochondrion; nucleus
>652-891/Domain: phage T4 DNA topoisomerase (ATP-hydrolyzing) medium chain homology <T4

Query Match 32.0%; Score 49; DB 2; Length 1239;
Best Local Similarity 36.0%; Pred. No. 43;
Matches 9; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

> 5 RYKFKVQGLDISIARLKTSMKFKVN 29
> 999 RRTQIGLLEMDLRLQSTKFKVEH 1023

>RESULT 7
>Plectin - human
>Species: Homo sapiens (man)
>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Aug-1999
>Accession: G02520
>McLean, W.H.I.; Smith, F.J.D.
>Submitted to the EMBL Data Library, March 1996
>Reference number: H01385
>Accession: G02520
>Status: preliminary; translated from GB/EMBL/DBJ
>Molecule type: mRNA
>Residues: 1-4574 <MCL>
>Cross-references: EMBL:U53204; NID:g1477645; PIDN:RAB05427.1; PID:g1477646
>Genetics:
>Gene: PLSCL
>Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein S
```

F;68-283/Domain: alpha-actinin actin-binding domain homology <ACT>

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Query Match 32.0%; Score 49; DB 2; Length 4574;
Best Local Similarity 45.5%; Pred. No. 1.6e+02;
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

> 4 GRYKFKVQGLDISIARLKTSMK 25
> 615 GAYRDCGLGRDLQYAKLLNSSK 636

>RESULT 8
>Plectin [imported] - human
>Species: Homo sapiens (man)
>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 19-Apr-2002
>Accession: C59404; A59404
>R; Liu, C.G.; Maercker, C.; Castanon, M.J.; Hauptmann, R.; Wiche, G.
>Proc. Natl. Acad. Sci. U.S.A. 93: 4278-4283, 1996
>Title: Human plectin: organization of the gene, sequence analysis, and chromosome loca
>Reference number: C59404; MUID:196210632; PMID:8633055
>Accession: C59404
>Status: preliminary
>Molecule type: DNA
>Residues: 1-4684 <STO>
>Cross-references: GB:CAA91196; NID:g1296662; PIDN:CAA91196.1
>Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein S
```

```
Query Match 32.0%; Score 49; DB 2; Length 4684;
Best Local Similarity 45.5%; Pred. No. 1.6e+02;
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

> 4 GRYKFKVQGLDISIARLKTSMK 25
> 725 GAYRDCGLGRDLQYAKLLNSSK 746
```

```
RESULT 9
>Plectin - rat
>Species: Rattus norvegicus (Norway rat)
>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
>Accession: A39638; S21876
>Wiche, G.; Becker, B.; Lubber, K.; Weitzer, G.; Castanon, M.J.; Hauptmann, R.; Stratowa
>J. Cell Biol. 114, 83-99, 1991
>Title: Cloning and sequencing of rat plectin indicates a 466-kD polypeptide chain with
>Reference number: A39638; MUID:91268156; PMID:2050743
>Accession: A39638
>Status: preliminary
>Molecule type: mRNA
>Residues: 1-4687 <WIC>
>Cross-references: EMBL:X59601; NID:g1292885; PIDN:CAA42169.1; PID:g1561642
>Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein S
>Keywords: cytoskeleton; transmembrane protein
>6-103/Domain: ribosomal protein S10 homology <RS10>
>184-399/Domain: alpha-actinin actin-binding domain homology <ACT>

Query Match 32.0%; Score 49; DB 1; Length 4687;
Best Local Similarity 45.5%; Pred. No. 1.6e+02;
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

> 4 GRYKFKVQGLDISIARLKTSMK 25
> 728 GAYRDCGLGRDLQYAKLLNSSK 749
```

```
RESULT 10
>Homocitrate synthase, alpha chain nifv(nioa) [imported] - Clostridium acetobutylicum
>Species: Clostridium acetobutylicum
>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
>Accession: G96931
>R; Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
```

; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A/Reference number: A96900; MUID:21359325; PMID:21359325
A/Accession: G96931
A>Status: preliminary
A/Molecule type: DNA
A/Residues: 1-265 <KUR>
A/Cross-references: GB:AE001437; PIDN:AAK78242.1; PID:G15023098; GSPDB:GN00168
A/Experimental source: Clostridium acetobutylicum ATCC824
C/Genetics:
A/Gene: CAC0261

Query Match 31.4%; Score 48; DB 2; Length 265;
Best Local Similarity 31.0%; Pred. No. 13;
Matches 9; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 1 CDCGRYKRVGQLDISIALKTSKMFVK 29
DB 229 CDFVAFNIIGTNRIDDLKLERMK 257

RESULT 11
A82211
MuCT/nudix family protein VC1342 [imported] - Vibrio cholerae (strain N16961 serogroup C
C/Species: Vibrio cholerae
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C/Accession: A82211
R;Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermlaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, E
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Accession: A82211
A>Status: preliminary
A/Molecule type: DNA
A/Residues: 1-465 <HEI>
A/Cross-references: GB:AE004214; GB:AE003852; NID:G9655832; PIDN:AAF94500.1; GSPDB:GN001
A/Experimental source: serogroup O1; strain N16961; biotype El Tor
C/Genetics:
A/Gene: VC1342
A/Map position: 1

Query Match 31.4%; Score 48; DB 2; Length 465;
Best Local Similarity 40.9%; Pred. No. 23;
Matches 9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 8 KRVGQLDISIALKTSKMFVK 29
DB 175 EWLGLQHGVQAKSKMPWLQN 196

RESULT 12
A95122
Tns252, relaxase [imported] - Streptococcus pneumoniae (strain TIGR4)
C/Species: Streptococcus pneumoniae
C/Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C/Accession: A95122
R;Hettlin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A/Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A/Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A/Reference number: A95000; MUID:21357209; PMID:11463916
A/Accession: A95122
A>Status: preliminary
A/Molecule type: DNA
A/Residues: 1-607 <KUR>
A/Cross-references: GB:AE005672; PIDN:AAK75170.1; PID:G14972530; GSPDB:GN00164; TIGR:SP4
A/Experimental source: strain TIGR4
C/Genetics:

A/Gene: SP1056

Query Match 31.4%; Score 48; DB 2; Length 607;
Best Local Similarity 52.4%; Pred. No. 30;
Matches 11; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 4 GRVKKFVGQLDISIALKTSK 24
DB 577 GRVKKVVRLLDKFNLNTGL 597

RESULT 13
G96998
Hypochemical protein CAC0802 [imported] - Clostridium acetobutylicum
C/Species: Clostridium acetobutylicum
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C/Accession: G96998
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A/Reference number: A96900; MUID:21359325; PMID:21359325
A/Accession: G96998
A>Status: preliminary
A/Molecule type: DNA
A/Residues: 1-358 <KUR>
A/Cross-references: GB:AE001437; PIDN:AAK78778.1; PID:G15023690; GSPDB:GN00168
A/Experimental source: Clostridium acetobutylicum ATCC824
C/Genetics:
A/Gene: CAC0802

Query Match 31.0%; Score 47.5; DB 2; Length 358;
Best Local Similarity 42.9%; Pred. No. 21;
Matches 12; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

QY 1 CDCGRYKRVGQLDISIALKTSKMFVK 28
DB 104 CKRGNKKIIGPVDAF-WLKRYMKINK 130

RESULT 14
AH1571
alpha-ribazole-5'-phosphatase homolog lin113 [imported] - Listeria innocua (strain Clif
C/Species: Listeria innocua
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 03-Nov-2003
C/Accession: AH1571
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karat, U.
Science 294, 849-852, 2001
A/Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A/Title: Comparative genomics of Listeria species
A/Reference number: AH1077; MUID:21537279; PMID:11679669
A/Accession: AH1571
A>Status: preliminary
A/Molecule type: DNA
A/Residues: 1-191 <GLA>
A/Cross-references: PIDN:CAC96344.1; PID:G16413572; GSPDB:GN00178
A/Experimental source: strain Clif11262
C/Genetics:
A/Gene: lin113
C/Superfamily: cofactor-dependent phosphoglycerate mutase; phosphoglycerate mutase homol

Query Match 30.7%; Score 47; DB 2; Length 191;
Best Local Similarity 37.5%; Pred. No. 13;
Matches 6; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 2 DCGRYKRVGQLDISI 17
DB 12 DCNALKKCYGQMDVAL 27

```

RESULT 15
C90026
Hypothetical protein narQ [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 07-Jul-2003
C:Accession: C90026
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
na, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Juncet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; PMID:21311952; PMID:11418146
A:Accession: C90026
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-265 <KUR>
A:Cross-references: GS:BA000018; FID:gl3702080; PIDN:BAB43372.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: narQ
S:Superfamily: formate dehydrogenase accessory protein FdhD

Query Match      30.7%; Score 47; DB 2; Length 265;
Best Local Similarity 54.5%; Pred. No. 19;
Matches 12; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

2Y      3  CGYRKVFVGQLDISIARLKISM 24
      |||: |||: |||: |||: |||:
Db      107  CGKSRFFVFQNDAAIA--KISM 126

Search completed: March 8, 2004, 12:16:20
Job time : 8.6652 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:02:31 ; Search time 61.3216 Seconds
(without alignments)
411.624 Million cell updates/sec

Title: US-09-600-932-2_COPY_148_227

Perfect score: 417

Sequence: 1 VIAGIRETEKFFYIVQEEK.....FIGVNDLEREGQVMFTDTP 80

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25;

1: sp_archaea;

2: sp_bacteria;

3: sp_fungi;

4: sp_human;

5: sp_invertebrate;

6: sp_mammal;

7: sp_mhc;

8: sp_organelle;

9: sp_phase;

10: sp_plant;

11: sp_rendent;

12: sp_virus;

13: sp_vertebrate;

14: sp_unclassified;

15: sp_rvirus;

16: sp_bacteriap;

17: sp_archaeap;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	417	100.0	277	4	Q9Y6Z7 homo sapien
2	405	97.1	277	11	Q8CF98
3	405	97.1	277	11	Q8CLC5 mus musculus
4	255	61.2	271	13	Q770T0
5	254	60.9	272	11	Q9DC75
6	250	60.0	268	4	Q7Z6N1
7	250	60.0	271	4	Q9BWP8
8	113.5	27.2	251	13	Q919Q8
9	106	25.4	238	13	Q57451
10	106	25.4	254	13	Q987R4
11	105	25.2	201	13	Q9DD44
12	103.5	24.8	1292	5	Q9DD44 Gallus gall
13	97	23.3	381	5	Q9VQ68
14	96	23.0	145	5	Q8WSW7
15	96	23.0	263	5	Q8WTP3
16	96	23.0	263	5	Q24696

17	93.5	22.4	222	13	Q90XB2
18	93.5	22.4	399	6	Q8HY12
19	93	22.3	246	13	Q919Q7
20	93	22.3	256	13	Q919Q9
21	90.5	21.7	404	6	Q8HY00
22	90.5	21.7	404	6	Q8HXZ9
23	90	21.6	208	11	Q91ZW7
24	89.5	21.5	399	6	Q8HY10
25	89	21.3	236	13	Q8UUM9
26	89	21.3	262	5	Q8WTP2
27	89	21.3	381	5	Q8WSW8
28	88.5	21.2	268	4	Q96QQ3
29	88.5	21.2	312	4	Q96Q07
30	88.5	21.2	334	4	Q96QP9
31	88.5	21.2	360	4	Q96Q04
32	88.5	21.2	380	4	Q96Q05
33	88.5	21.2	380	4	Q96Q00
34	88.5	21.2	404	4	Q96Q01
35	88.5	21.2	404	4	Q9NNX6
36	88.5	21.2	427	6	Q8HYB9
37	88	21.1	196	11	Q9EPW4
38	88	21.1	652	5	Q8WSX0
39	88	21.1	826	5	Q9VFS3
40	87.5	21.0	404	6	Q9SL98
41	87.5	21.0	422	6	Q8HY11
42	87.5	21.0	427	6	Q8HXZ7
43	87	20.9	163	13	Q8AXR8
44	86.5	20.7	312	6	Q8HXL6
45	86.5	20.7	381	6	Q95LC6

ALIGNMENTS

RESULT 1

Q9Y6Z7	PRELIMINARY;	PRT;	277 AA.
AC	Q9Y6Z7;		
DT	01-NOV-1999 (TREMBLrel. 12, Created)		
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)		
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)		
DE	Collectin 34.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=99240768; PubMed=10224141;		
RA	Ohtani K., Suzuki Y., Eda S., Kawai T., Kase T., Yamazaki H.,		
RA	Keeshi H., Sakai Y., Fukuhara A., Sakamoto T., Wakamiya N.,		
RT	"Molecular cloning of a novel collectin from liver (CL-Li).";		
RL	J. Biol. Chem. 274:13681-13689 (1999).		
DR	EMBL; AB002631; BAA81747.1; -		
DR	HSP; P19999; 2MSB.		
DR	Genew; HGNC:2220; COLEC10.		
DR	GO; GO:0005737; C:cytoplasm; TAS.		
DR	GO; GO:0005530; F:lectin; TAS.		
DR	InterPro; IPR008160; Collagen.		
DR	InterPro; IPR001304; Lactin_C.		
DR	Pfam; PF01391; Collagen; 1.		
DR	Pfam; PF00059; lectin c; 1.		
DR	SMART; SM00034; CLECT; 1.		
DR	PROSITE; PS00615; C TYPE LECTIN 1; 1.		
DR	PROSITE; PS00041; C TYPE LECTIN 2; 1.		
SQ	SEQUENCE 277 AA; 30733 MW; 9736861CEBDC5C25 CRC64;		

Query Match 100.0%; Score 417; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 7.2e-41;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VIAGIRETEKFFYIVQEEKYRESLTHCRIRGGMLAMPKDEANTLIADYVAKSGFRV 60

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Db 148 VIAGIRETEEFYIVQBEKNYRESLTHCRIRGGLAMPKDEAANTLIADYVAKSGFFRV 207
QY 61 FIGVNDLEREGQYMTDNT 80
Db 208 FIGVNDLEREGQYMTDNT 227

RESULT 2
Q8CF98 PRELIMINARY; PRT; 277 AA.
AC Q8CF98;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Collectin-J1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=22333927; PubMed=12450124;
RA Kawai T., Suzuki Y., Eda S., Kase T., Ohtani K., Sakai Y., Keshi H.,
RA Fukuoh A., Sakamoto T., Nozaki M., Copeland N.G., Jenkins N.A.,
RA Wakamiya N.;
RT "Molecular Cloning of Mouse Collectin Liver 1.";
RL Biosci. Biotechnol. Biochem. 66:2134-2145 (2002).
DR EMBL; AB016429; BAC3954.1; -
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF00059; lectin c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 277 AA; 30524 MW; 98C743A2E07A2872 CRC64;

Query Match 97.1%; Score 405; DB 11; Length 277;
Best Local Similarity 96.2%; Pred. No. 1.9e-39;
Matches 77; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VIAGIRETEEFYIVQBEKNYRESLTHCRIRGGLAMPKDEAANTLIADYVAKSGFFRV 60
Db 148 VIAGIRETEEFYIVQBEKNYRESLTHCRIRGGLAMPKDEAANTLIADYVAKSGFFRV 207

QY 61 FIGVNDLEREGQYMTDNT 80
Db 208 FIGVNDLEREGQYMTDNT 227

RESULT 3
Q8C1C5 PRELIMINARY; PRT; 277 AA.
AC Q8C1C5;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Collectin 34 homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
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DR EMBL; AK028423; BAC25941.1; -
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF00059; lectin c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 277 AA; 30510 MW; 94EF23A2E5404872 CRC64;

Query Match 97.1%; Score 405; DB 11; Length 277;
Best Local Similarity 96.2%; Pred. No. 1.9e-39;
Matches 77; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VIAGIRETEEFYIVQBEKNYRESLTHCRIRGGLAMPKDEAANTLIADYVAKSGFFRV 60
Db 148 VIAGIRETEEFYIVQBEKNYRESLTHCRIRGGLAMPKDEAANTLIADYVAKSGFFRV 207

QY 61 FIGVNDLEREGQYMTDNT 80
Db 208 FIGVNDLEREGQYMTDNT 227

RESULT 4
Q7TOT0 PRELIMINARY; PRT; 271 AA.
AC Q7TOT0;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
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QY      2   IAGIRETEKFFYYIVQEKNRYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFRFVF 61
Db      :|||:|||:|||:|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
144    VAVGRETESKIYLLVKEEKRYADAQLSCQARGGTLSMPKDEAANGLMAYLAQAQGLARVF 63

QY      62   IGVDNLEREGQYMETDNTTP 80
Db      |||:|||:|||:|||:|||:::|||||:::|||||:::|||||:::|||||
204    IGINDLEKEGAFVYSDRSP 222

RESULT 6
Q7Z6N1 PRELIMINARY; PRT; 268 AA.
AC Q7Z6N1.
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBurel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBurel. 25, Last annotation update)
MG3279 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
MEDLINE=22389257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner S.D., Collins F.S., Wagner L., Shennan C.W., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hate S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski W.I., Skalska U., Smalus D.E., Schnurch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RR "Generation and initial analysis of more than 15,000 full-length human
RRT and mouse cDNA sequences."
RRL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RRI [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strauberg R.;
RRL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RRI EMBL; BC009951; AAA09951.1; -.
RSR SEQUENCE 268 AA; 29005 MW; 30C3CC8C258AA9B7 CRC64;

Query Match 60.0%; Score 250; DB 4; Length 268;
Best Local Similarity 55.7%; Pred.No.3.6e-21;
Matches 44; Conservative 20; Mismatches 15; Indels 0; Gaps 0

QY      2   IAGIRETEKFFYYIVQEKNRYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFRFVF 61
Db      :|||:|||:|||:|||::~:|||||:::|||||:::|||||:::|||||:::|||||
140    VAVGRETESKIYLLVKEEKRYADAQLSCQARGGTLSMPKDEAANGLMAYLAQAQGLARVF 199

QY      62   IGVDNLEREGQYMTONTTP 80
Db      |||:|||:|||:|||:|||:::|||||:::|||||:::|||||:::|||||
200    IGINDLEKEGAFVISOHSP 218

RESULT 7
Q9BWP8 PRELIMINARY; PRT; 271 AA.
AC Q9BWP8.
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBurel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBurel. 25, Last annotation update)

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DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC000078; AAH00078.1; -.
DR HSSP; P22897; 1EG3.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 271 AA; 28665 MW; A14248CE41DB340 CRC64;

Query Match 60.0%; Score 250; DB 4; Length 271;
Best Local Similarity 55.7%; Pred. No. 3.6e-21;
Matches 44; Conservative 20; Mismatches 15; Indels 0; Gaps 0;

QY 2 IAGIRETEKFFYIVQEEKNYRSLTHCRIRGGMAMPKDEAANTLIADYVAKSGFFRVF 61
Db 143 VAGVRETSKIYLVKEKRYADQLSCQGGTSLPKDEANGLXAYLAQAGLARVF 202
QY 62 IGVNDLREGQVMTDNTF 80
Db 203 IGINDLEKGFVYSDHSP 221

RESULT 8
Q9I908 PRELIMINARY; PRT; 251 AA.
AC Q9I908;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mannose binding-like lectin precursor.
GN MBL
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20456722; PubMed=11003389;
RA Vitved L., Holmskov U., Koch C., Teisner B., Hansen S., Skjold K.;
RT "The homologue of mannose-binding lectin in the carp family Cyprinidae
is expressed at high level in spleen, and the deduced primary
structure predicts affinity for galactose."
RL Immunogenetics 51:955-964(2000).
DR EMBL; AF227738; BAF63469.1; -.
DR HSSP; P19999; IAFB.
DR ZFIN; ZDB-GENE-000427-2; mbl.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR008161; Clg_helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF01391; Collagen; 2.
DR Pfam; PF00059; lectin_c; 1.
DR ProDom; PD000007; Clg_helix; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
KW Collagen; Lectin; Signal.

FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 251 MANNOSE BINDING-LIKE LECTIN.
FT VARIANT 21 M -> L.
FT VARIANT 204 K -> N.
SQ SEQUENCE 251 AA; 26829 MW; 12DOABD06B6E3B11 CRC64;

Query Match 27.2%; Score 113.5; DB 13; Length 251;
Best Local Similarity 30.6%; Pred. No. 4.2e-05;
Matches 22; Conservative 20; Mismatches 29; Indels 1; Gaps 1;

QY 6 RETBEKFFYIVQEEKNYRSLTHCRIRGGMAMPKDEAANTLIADYVAKSGFFRVFIGN 65
Db 131 KVGQKYVTVDDVEETFDKGMQYCSSNGGALVLPRTLEENALLKVFVS-SAFKRLFIRIT 189
QY 66 DLREEGQVMTD 77
Db 190 DREKGEFVDID 201

RESULT 9
Q57451 PRELIMINARY; PRT; 238 AA.
ID Q57451
AC Q57451
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mannan-binding lectin (Fragment).
GN CMBL
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White Leghorn; TISSUE=Liver;
RA Laursen S.B.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF022226; AAB94071.1; -.
DR HSSP; P19999; IYTT.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR008161; Clg_helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF00059; lectin_c; 1.
DR ProDom; PD000007; Clg_helix; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
KW Collagen; Lectin.
FT NON_TER 238
SQ SEQUENCE 238 AA; 25645 MW; E5C9B5197AAE64E3 CRC64;

Query Match 25.4%; Score 106; DB 13; Length 238;
Best Local Similarity 28.2%; Pred. No. 0.00031;
Matches 20; Conservative 20; Mismatches 29; Indels 2; Gaps 1;

QY 10 EKFFYIVQEEKNYRSLTHCRIRGGMAMPKDEAANTLIADYVAKSGFFRVFIGNDLER 69
Db 126 KMFVSTGKYNFEKSKLCAKAGSVLAFRNEAENTALKDLIDFSS--QAYIGISDAQT 183
QY 70 EGQVMTDNTF 80
Db 184 EGRFMYLSGGP 194

RESULT 10
Q98TA4 PRELIMINARY; PRT; 254 AA.
ID Q98TA4
AC Q98TA4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)

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DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mannose-binding lectin protein precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OK NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20456722; PubMed=11003389;
RA Vitved L., Holmskov U., Koch C., Telsner B., Hansen S., Skjoldt K.;
RT "The homologue of mannose-binding lectin in the carp family Cyprinidae
RT is expressed at high level in spleen, and the deduced primary
RT structure predicts affinity for galactose.";
RL Immunogenetics 51:955-964(2000).
DR EMBL; AF231714; AAK30298.1; -.
DR HSSP; P19999; 1YTT.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008161; Clg helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR000005; HTHArac.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF00059; lectin_C; 1.
DR ProDom; PD000007; Clg_helix; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
KW Collagen; Lectin; Signal.
FT SIGNAL 1 21
FT CHAIN 22 254
FT VARIAT 234 234 D -> V.
FT SEQUENCE 254 AA; 27376 MW; C924428643441AED CRC64;

Query Match 25.4%; Score 106; DB 13; Length 254;
Best Local Similarity 28.2%; Pred. No. 0.00033;
Matches 20; Conservative 20; Mismatches 29; Indels 2; Gaps 1;

QY 10 EKFYIVQEEKNYRESLTHCRIRGGMLAMPKRAANTLIADYVAKSGFFRVFTGVNDLER 69
DB 142 KMFVSTGKKYFKGSLCAKAGSVLSPRNEANTALKDLIDPS--QAVIGISDAQT 199
QY 70 EGQYMTDNT 80
DB 200 EGFWYLSGGP 210

RESULT 11
Q9DDD4 PRELIMINARY; PRT; 201 AA.
AC Q9DDD4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tetraectin.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OK NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20456722; PubMed=11003389;
RA Vitved L., Holmskov U., Koch C., Telsner B., Hansen S., Skjoldt K.;
RT "The homologue of mannose-binding lectin in the carp family Cyprinidae
RT is expressed at high level in spleen, and the deduced primary
RT structure predicts affinity for galactose.";
RL Immunogenetics 51:955-964(2000).
DR EMBL; AF231714; AAK30298.1; -.
DR HSSP; P19999; 1YTT.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008161; Clg helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR000005; HTHArac.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF00059; lectin_C; 1.
DR ProDom; PD000007; Clg_helix; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
KW Collagen; Lectin; Signal.
FT SIGNAL 1 21
FT CHAIN 22 254
FT VARIAT 234 234 D -> V.
FT SEQUENCE 254 AA; 27376 MW; C924428643441AED CRC64;
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DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pancreatin_ac.
DR Pfam; PF00059; lectin_C; 1.
DR PRINTS; PR01504; PNCREATITSP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
DR SEQUENCE 201 AA; 22172 MW; 7C7F235D24426AE8 CRC64;

Query Match 25.2%; Score 105; DB 13; Length 201;
Best Local Similarity 30.6%; Pred. No. 0.00033;
Matches 22; Conservative 15; Mismatches 33; Indels 2; Gaps 1;

QY 11 KFYIVQEEKNYRESLTHCRIRGGMLAMPKRAANTLIADYVAKS--GFFRVFTGVNDLE 68
DB 79 KCFLAPSEKTYHEASEHCISQGGTLGTQGGENDALDYMKRSIGNAEIWLGLNDWV 138
QY 69 REGQYMTDNT 80
DB 139 AEGKWVDMTGSP 150

RESULT 12
Q9VQ68 PRELIMINARY; PRT; 1292 AA.
AC Q9VQ68;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CG15378 protein.
GN LECTIN-22C OR CG15378.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OK NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blasej R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Fabios B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flesler C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hestlin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mirkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Kusekern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
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RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003584; AAF51313.1; -.
DR HSSP; P05452; 1TN3.
DR FlyBase; FBgn040105; lectin-22C.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin bind_Pera.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF01607; CBM_14; 3.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00494; ChtBD2; 3.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C-TYPE LECTIN 2; 1.
SQ SEQUENCE 1292 AA; 142942 MW; 327C0F3968B2BBC8 CRC64;

Query Match 24.8%; Score 103.5; DB 5; Length 1292;
Best Local Similarity 34.7%; Pred. No. 0.0043;
Matches 25; Conservative 15; Mismatches 29; Indels 3; Gaps 2;

QY 4 GIRETEEFYIVQ-EEKNYRESLTHCRIRGGLAMPKDEAANTLIADYVAKSGFFRVFI 62
Db 138 GFEQIGSKYVIEKYSEKNSWSTASKCNMGHLADIKDEADLAIAKANLKEDTHY--WL 195

QY 63 GYNDLEREQYM 74
Db 196 GINDLDHEGKFL 207

RESULT 13
Q8WSW7 PRELIMINARY; PRT; 381 AA.
AC Q8WSW7; (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Scarf3b.
GN SCARF3B.
OS Dugesia tigrina (Planarian).
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC Paludicola; Dugesidae; Girardia.
OX NCBI_TaxID=6162;
RN [1]
RP SEQUENCE FROM N.A.
RA Bogdanova E.A., Shagin D., Lukyanov K.A., Barsova E.V., Punkova N.,
RA Usman N., Matz M., Gurskaya N., Lukyanov S.A.;
RT "Characterization of a novel family of C-type lectin proteins from
Planaria entitled multi-domain free lectins.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057977; AAL29935.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 3.
DR SMART; SM00034; CLECT; 3.
DR PROSITE; PS00615; C-TYPE LECTIN 1; 3.
DR PROSITE; PS50041; C-TYPE LECTIN 2; 3.
SQ SEQUENCE 381 AA; 43996 MW; F34922A2B17FA87F CRC64;

Query Match 23.3%; Score 97; DB 5; Length 381;
Best Local Similarity 23.3%; Pred. No. 0.0061;
Matches 17; Conservative 22; Mismatches 34; Indels 0; Gaps 0;

QY 8 TEKFPYIVQSEKNYRESLTHCRIRGGLAMPKDEAANTLIADYVAKSGFFRVFIGNDL 67
Db 17 TQACYHLNKNKNYNDVAVKYNSEKRLVKITDSQTNAAVFELASKNGMGTYWNGNDI 76

QY 68 EREGQYMTDNT 80
Db 77 AIEGTWVDENK 89

RESULT 14
Q8WSW6 PRELIMINARY; PRT; 145 AA.
AC Q8WSW6; (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Scarf1.
GN SCARF1.
OS Dugesia tigrina (Planarian).
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC Paludicola; Dugesidae; Girardia.
OX NCBI_TaxID=6162;
RN [1]
RP SEQUENCE FROM N.A.
RA Bogdanova E.A., Shagin D., Lukyanov K.A., Barsova E.V., Punkova N.,
RA Usman N., Matz M., Gurskaya N., Lukyanov S.A.;
RT "Characterization of a novel family of C-type lectin proteins from
Planaria entitled multi-domain free lectins.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057980; AAL29937.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.
DR PROSITE; PS50041; C-TYPE LECTIN 2; 1.
SQ SEQUENCE 145 AA; 16670 MW; 3D1337BBE477CB25 CRC64;

Query Match 23.0%; Score 96; DB 5; Length 145;
Best Local Similarity 23.3%; Pred. No. 0.0026;
Matches 17; Conservative 22; Mismatches 34; Indels 0; Gaps 0;

QY 8 TEKFPYIVQSEKNYRESLTHCRIRGGLAMPKDEAANTLIADYVAKSGFFRVFIGNDL 67
Db 17 TQACYHLNKNKNYNDVAVKYNSEKRLVKITDSQTNAAVFELASKNGMGTYWNGNDI 76

QY 68 EREGQYMTDNT 80
Db 77 AIEGTWVDENK 89

RESULT 15
Q8WTF3 PRELIMINARY; PRT; 263 AA.
AC Q8WTF3; (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Scarf2.
GN SCARF2.
OS Dugesia tigrina (Planarian).
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC Paludicola; Dugesidae; Girardia.
OX NCBI_TaxID=6162;
RN [1]
RP SEQUENCE FROM N.A.
RA Bogdanova E.A., Shagin D., Lukyanov K.A., Barsova E.V., Punkova N.,
RA Usman N., Matz M., Gurskaya N., Lukyanov S.A.;
RT "Inductive interactions regulating body patterning in planarian,
revealed by analysis of expression of novel gene scarf.";
RL Dev. Biol. 194:172-181(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Bogdanova E.A., Shagin D., Lukyanov K.A., Barsova E.V., Punkova N.,
RA Usman N., Matz M., Gurskaya N., Lukyanov S.A.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057975; AAL29933.1; -.

Db 77 AIEGTWVDENK 89

RESULT 14
Q8WSW6 PRELIMINARY; PRT; 145 AA.
AC Q8WSW6; (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Scarf1.
GN SCARF1.
OS Dugesia tigrina (Planarian).
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC Paludicola; Dugesidae; Girardia.
OX NCBI_TaxID=6162;
RN [1]
RP SEQUENCE FROM N.A.
RA Bogdanova E.A., Shagin D., Lukyanov K.A., Barsova E.V., Punkova N.,
RA Usman N., Matz M., Gurskaya N., Lukyanov S.A.;
RT "Characterization of a novel family of C-type lectin proteins from
Planaria entitled multi-domain free lectins.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057980; AAL29937.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.
DR PROSITE; PS50041; C-TYPE LECTIN 2; 1.
SQ SEQUENCE 145 AA; 16670 MW; 3D1337BBE477CB25 CRC64;

Query Match 23.0%; Score 96; DB 5; Length 145;
Best Local Similarity 23.3%; Pred. No. 0.0026;
Matches 17; Conservative 22; Mismatches 34; Indels 0; Gaps 0;

QY 8 TEKFPYIVQSEKNYRESLTHCRIRGGLAMPKDEAANTLIADYVAKSGFFRVFIGNDL 67
Db 17 TQACYHLNKNKNYNDVAVKYNSEKRLVKITDSQTNAAVFELASKNGMGTYWNGNDI 76

QY 68 EREGQYMTDNT 80
Db 77 AIEGTWVDENK 89

RESULT 15
Q8WTF3 PRELIMINARY; PRT; 263 AA.
AC Q8WTF3; (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Scarf2.
GN SCARF2.
OS Dugesia tigrina (Planarian).
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC Paludicola; Dugesidae; Girardia.
OX NCBI_TaxID=6162;
RN [1]
RP SEQUENCE FROM N.A.
RA Bogdanova E.A., Shagin D., Lukyanov K.A., Barsova E.V., Punkova N.,
RA Usman N., Matz M., Gurskaya N., Lukyanov S.A.;
RT "Inductive interactions regulating body patterning in planarian,
revealed by analysis of expression of novel gene scarf.";
RL Dev. Biol. 194:172-181(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Bogdanova E.A., Shagin D., Lukyanov K.A., Barsova E.V., Punkova N.,
RA Usman N., Matz M., Gurskaya N., Lukyanov S.A.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057975; AAL29933.1; -.

Result No.	Query	Score	Match	Length	DB	ID	Description
1	91	21.8	166	1	TETN_CARP	P26258	carcharhinu
2	85	20.4	197	1	CL61_HUMAN	P75596	homo sapien
3	83.5	20.0	369	1	PSPD_BOVIN	P35246	bos taurus
4	82	19.5	202	1	TETN_HUMAN	P05452	homo sapien
5	81.5	19.5	321	1	CL43_BOVIN	P42916	bos taurus
6	81.5	19.5	371	1	CL46_BOVIN	Q8mh29	bos taurus
7	81.5	19.5	1456	1	MANR_HUMAN	P22897	homo sapien
8	79.5	19.1	374	1	PSPD_MOUSE	P50404	mus musculus
9	78.5	18.8	248	1	PSPA_HUMAN	P07714	homo sapien
10	78	18.7	202	1	TETN_MOUSE	P43025	mus musculus
11	78	18.7	328	1	SCGF_HUMAN	O88200	mus musculus
12	78	18.7	328	1	SCGF_RAT	O88201	rattus norv
13	77.5	18.6	550	1	KUCR_RAT	P10716	rattus norv
14	76.5	18.3	371	1	CONG_BOVIN	P23805	bos taurus
15	76.5	18.3	548	1	KUCR_MOUSE	P70194	mus musculus
16	74	17.7	238	1	MABA_RAT	P19999	rattus norv
17	73.5	17.6	155	1	PLC_FALLA	P82596	halloctis la
18	72	17.5	1722	1	LY75_HUMAN	O60449	homo sapien
19	72	17.3	323	1	SCGF_HUMAN	Q9Y240	homo sapien
20	71.5	17.1	374	1	PSPD_RAT	P35248	rattus norv
21	71.5	17.1	1450	1	SREJ_STRPU	Q26627	strongyloce
22	70.5	16.9	331	1	FCB2_MOUSE	P20593	mus musculus
23	70.5	16.9	1458	1	PA2R_PABIT	P49260	oryctolagus
24	69.5	16.7	162	1	LEC3_MEGHO	P07439	megabalanus
25	69.5	16.7	1463	1	PA2R_BOVIN	P49259	bos taurus
26	69	16.5	828	1	MARC_KLEPN	P21647	klebsiella
27	67.5	16.2	247	1	PSPA_CAVPO	P50403	cavia porce
28	66.5	15.9	375	1	PSPD_HUMAN	P35247	homo sapien
29	66.5	15.9	872	1	TR95_TETHH	Q94819	tetrahymena
30	66	15.8	249	1	MABC_BOVIN	O02559	bos taurus
31	65.5	15.7	628	1	FTSH_PORPU	P51327	porphyra pu
32	64.5	15.3	207	1	LECH_CHICK	P02707	gallus gall
33	64	15.3	746	1	TDCE_ECOLI	P42632	escherichia

RESULT 2			
CLEI HUMAN			
ID CLEI HUMAN	STANDARD;	PRT:	197 AA.
AC O75596;			
DT 28-FEB-2003	(Rel. 41, Created)		
DT 28-FEB-2003	(Rel. 41, Last sequence update)		

```

10-OCT-2003 (Rel. 42, Last annotation update)
C-type lectin superfamily member 1 precursor (Cartilage-derived C-type
lectin).
CLCSCF1.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=Cartilage;
MEDLINE=99453719; PubMed=10524194;
Neame P.J., Tapp H., Grimm D.R.;
"The cartilage-derived, C-type lectin (CLCSCF1): structure of the gene
and chromosomal location.";
Biochim. Biophys. Acta 1446:193-202(1999).
-!- TISSUE SPECIFICITY: Restricted to cartilage.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
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or send an email to license@isb-sib.ch).
EMBL; AF077345; AAD12542.1; -.
EMBL; AF077344; AAD12542.1; JOINED.
HSSP; P05452; IHTN.
Genew; HGNC:2052; CLCSCF1.
GO; GO:0005530; F:lectin; TAS.
GO; GO:0001501; P:skeletal development; TAS.
InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
Lectin; Signal.
CHAIN 1 22 POTENTIAL.
FT CHAIN 23 197 C-TYPE LECTIN SUPERFAMILY MEMBER 1.
FT DOMAIN 74 192 C-TYPE LECTIN.
FT DISULFID 68 78 BY SIMILARITY.
FT DISULFID 95 191 BY SIMILARITY.
FT DISULFID 167 183 BY SIMILARITY.
SEQUENCE 197 AA; 22232 MW; BB924DBDB7729A4 CRC64;

Query Match 20.4%; Score 85; DB 1; Length 197;
Best Local Similarity 25.7%; Pred. No. 0.016;
Matches 18; Conservative 20; Mismatches 30; Indels 2; Gaps 1;

2Y 7 ETEKFFYIVQEEKNYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKS--GFFRVFVIG 64
Db 73 KVHKCYLASGLGHFHEANEDCISKGLIVIPRNSDEINALQDYGRSLPGVDFWLGI 132
2Y 65 NDLREGQYIM 74
Db 133 NDMVTEGKFV 142

RESULT 3
2SPD_BOVIN
ID_PSPD_BOVIN STANDARD; PRT; 369 AA.
AC P35246;
JT 01-FEB-1994 (Rel. 28, Created)
JT 01-FEB-1994 (Rel. 28, Last sequence update)
JT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Pulmonary surfactant-associated protein D precursor (SP-D) (PSP-D).
EN SFTPD OR SFTPA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
```

```

OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 208-247.
RC TISSUE=Lung;
RX MEDLINE=93170856; PubMed=8436402;
RA Lim B.L., Lu J., Reid K.B.M.;
RT "Structural similarity between bovine conglutinin and bovine lung
RT surfactant protein D and demonstration of liver as a site of
RT synthesis of conglutinin.";
RL Immunology 78:159-165(1993).
CC -!- FUNCTION: Contributes to the lung's defense against inhaled
CC microorganisms. Binds strongly maltose residues and to a lesser
CC extent other alpha-glucosyl moieties. It could participate in the
CC extracellular reorganization or turnover of pulmonary surfactant.
CC -!- SUBUNIT: Oligomeric complex of 4 set of homotrimers.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- MISCELLANEOUS: Pulmonary surfactant consists of 90% lipid and 10%
CC protein. There are 4 surfactant-associated protein: 2 collagenous,
CC carbohydrate-binding glycoproteins (SP-A and SP-D) and 2 small
CC hydrophobic proteins (SP-B and SP-C).
CC -!- SIMILARITY: Contains 1 collagenous domain.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
EMBL; X75911; CAA53510.1; -.
HSSP; P35247; 1B08.
InterPro; IPR008160; Collagen.
InterPro; IPR001304; Lectin_C.
Pfam; PF01391; Collagen; 2.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
Glycoprotein; Calcium; Surface film; Gaseous exchange; Hydroxylation;
Signal; Lectin; Collagen; Repeat; Coiled coil.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 369 PULMONARY SURFACTANT-ASSOCIATED PROTEIN
FT D.
FT DOMAIN 46 216 COLLAGEN-LIKE.
FT DOMAIN 217 248 COILED COIL (POTENTIAL).
FT DOMAIN 273 369 C-TYPE LECTIN (SHORT FORM).
FT DISULFID 275 367 BY SIMILARITY.
FT DISULFID 345 359 BY SIMILARITY.
FT CARBOHYD 90 90 N-LINKED (GLCNAC...) (POTENTIAL).
FT MOD_RES 78 78 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 87 87 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 96 96 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 99 99 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 165 165 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 171 171 HYDROXYLATION (BY SIMILARITY).
SEQUENCE 369 AA; 37361 MW; 07D8B24E0AEB2E3 CRC64;

Query Match 20.0%; Score 83.5; DB 1; Length 369;
Best Local Similarity 25.3%; Pred. No. 0.048;
Matches 19; Conservative 16; Mismatches 39; Indels 1; Gaps 1;

QY 6 RETEEKFYIVQEEKNYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFFRVFVIGN 65
Db 252 RSVGEKIFKTVGSEKTFQDAQOICIQAGQLPSPRSGAENALIQ-LATAQNKAAFLSMS 310
QY 66 DLREGQYIMTDNTP 80
Db 311 DTRKEGTFIVPTGEP 325

RESULT 4
```

TEIN HUMAN
ID TETN HUMAN STANDARD; PRT; 202 AA.
AC P05452;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tetranectin precursor (TN) (Plasminogen-kringle 4 binding protein).
GN TNA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=92365345; PubMed=1354271;
RA Wewer U.M.; Albrechtsen R.;
RT "Tetranectin, a plasminogen kringle 4-binding protein. Cloning and
RT gene expression pattern in human colon cancer.";
RL Lab. Invest. 67:253-262(1992).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=92380263; PubMed=1511740;
RA Berglund L.; Petersen T.E.;
RT "The gene structure of tetranectin, a plasminogen binding protein.";
RL FEBS Lett. 309:15-19(1992).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.,
RA Klausner R.D.; Collins F.S.; Wagner C.M.; Shenmen C.M.; Schuler G.D.,
RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.,
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.,
RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.,
RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Schetz T.E.,
RA Brownstein M.J.; Usdin T.B.; Toshiyuki S.; Carninci P.; Prange C.,
RA Rana S.S.; Loquellano I.A.; Peters G.J.; Abramson R.D.; Mullany S.J.,
RA Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.,
RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.,
RA Villalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.,
RA Fahey J.; Helton E.; Kettaman M.; Madan A.; Rodrigues S.; Sanchez A.,
RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.,
RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.,
RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.,
RA Butterfield Y.S.N.; Krzywinski M.I.; Skalska U.; Smailus D.E.,
RA Schnerch A.; Schein J.E.; Jones S.J.M.; Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[4]
RP SEQUENCE OF 22-202, AND VARIANTS SER-55 AND MET-58.
RX MEDLINE=88107595; PubMed=3427041;
RA Fuhlendorff J.; Clemmensen I.; Magnusson S.;
RT "Primary structure of tetranectin, a plasminogen kringle 4 binding
RT plasma protein: homology with asialoglycoprotein receptors and
RT cartilage proteoglycan core protein.";
RL Biochemistry 26:6757-6764(1987).
[5]
RP SEQUENCE OF 1-36 FROM N.A.
RC TISSUE=Placenta;
RX Sorensen C.B.; Berglund L.; Petersen T.E.;
RT "Cloning and mapping of the murine tetranectin gene.";
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
[6]
RP PARTIAL SEQUENCE, MASS SPECTROMETRY, AND VARIANT GLY-106.
RX MEDLINE=20080486; PubMed=10614823;
RA Jaquinod M.; Holtet T.L.; Etzerodt M.; Clemmensen I.; Thøgersen H.C.,
RA Roepstorff P.;
RT "Mass spectrometric characterisation of post-translational
RT modification and genetic variation in human tetranectin.";
RL Biol. Chem. 380:1307-1314(1999).

[7]
RN RP X-RAY CRYSTALLOGRAPHY (2.8 ÅNGSTRÖMS).
RX MEDLINE=97398360; PubMed=9256258;
RA Nielsen B.B.; Kastrup J.S.; Rasmussen H.; Holtet T.L.; Graversen J.H.,
RA Etzerodt M.; Thøgersen H.C.; Larsen I.K.;
RT "Crystal structure of tetranectin, a trimeric plasminogen-binding
RT protein with an alpha-helical coiled coil.";
RL FEBS Lett. 412:388-396(1997).
[8]
RN RP X-RAY CRYSTALLOGRAPHY (2.0 ÅNGSTRÖMS) OF 66-202.
RX MEDLINE=98437604; PubMed=9757090;
RA Kastrup J.S.; Nielsen B.B.; Rasmussen H.; Holtet T.L.; Graversen J.H.,
RA Etzerodt M.; Thøgersen H.C.; Larsen I.K.;
RT "Structure of the C-type lectin carbohydrate recognition domain of
RT human tetranectin.";
RL Acta Crystallogr. D 54:757-766(1998).
CC -!- FUNCTION: Tetranectin binds to plasminogen and to isolated kringle
CC 4. May be involved in the packaging of molecules destined for
CC exocytosis.
CC -!- SUBUNIT: Homotrimer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Found in plasma.
CC -!- MASS SPECTROMETRY: MW=20535.8; MW_ERR=2.4; METHOD=Electrospray;
CC RANGE=22-202.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC
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CC
CC EMBL; X70910; CAAS0285.1; --
CC EMBL; X70911; CAAS0285.1; JOINED.
CC EMBL; X70912; CAAS0285.1; JOINED.
CC EMBL; X64559; CAAS0285.1; --
CC EMBL; BC011024; AAH11024.1; --
CC EMBL; X98121; CAAG6803.1; --
CC PIR; S24126; TTHUN
CC PDB; 1HTN; 03-DEC-97.
CC PDB; 1TN3; 06-MAY-98.
CC Genew; HGNC:11891; TNA.
CC MIN; 187520; --
CC GO; GO:0001501; P:skeletal development; TAS.
CC InterPro; IPR001304; LECTIN_C.
CC InterPro; IPR003990; Pancreatins_ac.
CC Pfam; PF00059; lectin_c; 1.
CC PRINTS; PR01504; PNCREATINSAP.
CC SMART; SM00034; CLECT; 1.
CC PROSITE; PS00615; C TYPE LECTIN 1; 1.
CC PROSITE; PS00041; C TYPE LECTIN 2; 1.
CC LECTIN; Plasma; Signal; Polymorphism; Glycoprotein; 3D-structure.
FT SIGNAL 1 21
FT CHAIN 22 202
FT DOMAIN 77 198
FT DISULFID 71 81
FT DISULFID 98 137
FT DISULFID 173 189
FT CARBOHYD 25 25
FT VARIANT 55 55
FT VARIANT 58 58
FT VARIANT 106 106
FT STRAND 70 73
FT STRAND 79 89
FT HELIX 91 100
FT TURN 101 102
FT STRAND 104 105
FT HELIX 111 124
O-LINKED (GALNAc. . .).
A -> S.
V -> M.
/FTID=VAR_004189.
/FTID=VAR_004190.
S -> G (in dBSNP:13963).
/FTID=VAR_012318.

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FT TURN 125 125
FT TURN 127 128
FT STRAND 130 140
FT TURN 140 140
FT TURN 141 142
FT STRAND 143 146
FT TURN 147 148
FT STRAND 151 151
FT STRAND 157 157
FT TURN 160 162
FT HELIX 168 170
FT STRAND 173 177
FT TURN 178 182
FT STRAND 183 187
FT TURN 189 190
FT STRAND 193 200
FT SEQUENCE 202 AA; 22567 MW; 2B0DCB5DF22E1AB8 CRC64;

Query Match 19.7%; Score 82; DB 1; Length 202;
Best Local Similarity 25.8%; Pred. No. 0.036;
Matches 17; Conservative 18; Mismatches 29; Indels 2; Gaps 1;

QY 11 KFYIVQEEKYRSLTHCRIRGKMLAMPKDEAANTLIADYVKS--GFRFVFIGVNDLE 68
DB 80 KCFLAFTQTKTFHEASEDCISRGGTLSTPQTGSENDALVEYLRSQVGNRAEIVLGLNDMA 139
QY 69 REGQYMF 74
DB 140 REGTIV 145

RESULT 5
CL43_BOVIN STANDARD; PRT; 321 AA.
AC P42916; OHMF4;
DT 01-NOV-1995 (Rel. 32, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Collectin-43 precursor (CL-43) (43 kDa collectin).
GN CL43.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22414671; PubMed=12527419;
RA Hansen S., Holm D., Moeller V., Vitved L., Bendixen C., Skjodt K.,
RA Holmskov U.;
RT "Genomic and molecular characterization of CL-43 and its proximal
RT promoter.";
RL Biochim. Biophys. Acta 1625:1-10(2003).
RN [2]
RP SEQUENCE OF 21-321 FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94216283; PubMed=8163480;
RA Lim B.-L., Willis A.C., Reid K.B.M., Lu J., Laursen S.B.,
RA Jensenius J.C., Holmskov U.;
RT "Primary structure of bovine collectin-43 (CL-43). Comparison with
RT conglutinin and lung surfactant protein-D.";
RL J. Biol. Chem. 269:11820-11824(1994).
CC -!- FUNCTION: Lectin that binds to various sugars: mannose >
CC fucose > galNAc > glucose > maltose > galactose > lactose >
CC gainac. Could play a role in immune defense.
CC -!- SUBUNIT: Oligomeric complex of 4 set of homotrimers.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Liver specific.
CC -!- PTM: Hydroxylated (Potential).
CC -!- SIMILARITY: Contains 1 collagenous domain.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
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CC -----
DR EMBL; AY071821; AAL61855.1; -.
DR EMBL; AY071822; AAL61856.1; -.
DR EMBL; X75912; CAA53511.1; ALT_SEQ.
DR HSSP; P35247; IB08.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR01304; Lectin_C.
DR Pfam; PF01391; Collagen; 2.
DR Pfam; PF00059; Lectin_C; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.
DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.
KW Lectin; Hydroxylation; Glycoprotein; Mannose-binding; Collagen;
KW Repeat; Calcium; signal.
FT SIGNAL 1 20
FT CHAIN 21 321 COLLECTIN-43.
FT DOMAIN 49 162 COLLAGEN-LIKE.
FT DOMAIN 222 321 C-TYPE LECTIN (SHORT FORM).
FT DISULFID 224 319 BY SIMILARITY.
FT DISULFID 297 311 BY SIMILARITY.
FT CONFLICT 125 125 T -> A (IN REF. 2).
FT CONFLICT 286 286 N -> G (IN REF. 2).
SQ SEQUENCE 321 AA; 33615 MW; 12BF120BB4861A1 CRC64;

Query Match 19.5%; Score 81.5; DB 1; Length 321;
Best Local Similarity 28.4%; Pred. No. 0.069;
Matches 19; Conservative 15; Mismatches 30; Indels 3; Gaps 2;

QY 10 KFYIVQEEKYRSLTHCRIRGKMLAMPKDEAANTLIADYV-AKSGFRFVFIGVNDLE 68
DB 205 EKIFTAGVKSYSDAEQLCRAKQGLASPRSSAENAVTQVRAKKV--HAYLSMNDIS 262
QY 69 REGQYMF 75
DB 263 KEGKFTV 269

RESULT 6
CL46_BOVIN STANDARD; PRT; 371 AA.
AC Q8MHZ9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Collectin-46 precursor (CL-46) (46 kDa collectin).
GN CL46.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Hansen S., Holm D., Moeller V., Vitved L., Bendixen C., Reid K.B.M.,
RA Skjodt K., Holmskov U.;
RT "CL-46, a novel collectin highly expressed in the bovine thymus and
RT liver.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SUBUNIT: Oligomeric complex of 4 set of homotrimers (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Highly expressed in thymus and liver.
CC -!- PTM: Hydroxylated (Potential).
CC -!- SIMILARITY: Contains 1 collagenous domain.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
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CC EMBL; AF509589; AAM34742.1; -
DR EMBL; AF509590; AAM34743.1; -
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; LECTIN_C.
DR Pfam; PF01391; Collagen; 2.
DR Pfam; PF00059; lectin c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 2; 1.
KW LECTIN; Hydroxylation; Glycoprotein; Mannose-binding; Membrane;
KW Collagen; Repeat; Calcium; Signal.
FT SIGNAL 1 20
FT CHAIN 21 371
FT DOMAIN 46 216
FT DOMAIN 273 371
FT SITE 201 203
FT DISULFID 275 369
FT DISULFID 347 361
FT CARBOHYD 90 90
SQ SEQUENCE 371 AA; 37445 MW; 108AC45A91420E83 CRC64;

Query Match 19.5%; Score 81.5; DB 1; Length 371;
Best Local Similarity 29.9%; Pred. No. 0.081;
Matches 20; Conservative 14; Mismatches 30; Indels 3; Gaps 2;

QY 10 EKPYIVIOEKNYRESLTHCRIGRMGLAMPDEAAANTLIADYV-AKSGFFRFVIGNDLE 68
Db 256 KIKFTAGVKSYSQAQOLCREAKGQLASPSRAEAEVAQLVRKXN--DAFLSNWDIS 313
QY 69 REGQYMF 75
Db 314 TEGKFTY 320

RESULT 7

ID MANR HUMAN STANDARD; PRT; 1456 AA.
AC P22897;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Macrophage mannose receptor precursor (MWR) (CD206 antigen).
GN MRC1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=90324192; PubMed=2373685;
RA Taylor M.E., Conary J.T., Lennartz M.R., Stahl P.D., Drickamer K.;
RT "Primary structure of the mannose receptor contains multiple motifs
RT resembling carbohydrate-recognition domains.";
RL J. Biol. Chem. 265:12156-12162 (1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93052405; PubMed=1294118;
RA Kim S.J., Ruiz N., Bezouska K., Drickamer K.;
RT "Organization of the gene encoding the human macrophage mannose
RT receptor (MRC1).";
RL Genomics 14:721-727 (1992).
RN [3]
RP STUDIES ON THE BINDING OF INDIVIDUAL LECTIN DOMAINS.
RX MEDLINE=92112893; PubMed=1730714;
RA Taylor M.E., Bezouska K., Drickamer K.;

"Contribution to ligand binding by multiple carbohydrate-recognition
domains in the macrophage mannose receptor.";
J. Biol. Chem. 267:1719-1726 (1992).
[4]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 642-788.
RA MEDLINE=20347275; PubMed=10779515;
RX Feinberg H., Park-Snyder S., Kolatkar A.R., Heise C.T., Taylor M.E.,
RA Weiss W.I.;
RT "Structure of a C-type carbohydrate recognition domain from the
RT macrophage mannose receptor.";
RL J. Biol. Chem. 275:21539-21548 (2000).
CC -!- FUNCTION: Mediates the endocytosis of glycoproteins by
CC macrophages, in several recognition and uptake processes.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- MISCELLANEOUS: CRDs 1-3 have at most very weak affinity for
CC carbohydrate. CRD 4 shows the highest affinity binding and has
CC multispecificity for a variety of monosaccharides. At least 3 CRDs
CC (4, 5, and 7) are required for high affinity binding and
CC endocytosis of multivalent glycoconjugates.
CC -!- SIMILARITY: Contains 8 C-type lectin family domains.
CC -!- SIMILARITY: Contains 1 ricin B-type lectin domain.
CC -!- DATABASE: NAME=PROW; NOTE=PROW 2:85-89 (2001);
CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/1644341535_g.htm".

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CC or send an email to license@isb-sib.ch).

EMBL; J05550; AAA59868.1; -
EMBL; M93221; AAA60389.1; -
DR EMBL; M93192; AAA60389.1; JOINED.
DR EMBL; M93193; AAA60389.1; JOINED.
DR EMBL; M93194; AAA60389.1; JOINED.
DR EMBL; M93195; AAA60389.1; JOINED.
DR EMBL; M93196; AAA60389.1; JOINED.
DR EMBL; M93197; AAA60389.1; JOINED.
DR EMBL; M93198; AAA60389.1; JOINED.
DR EMBL; M93199; AAA60389.1; JOINED.
DR EMBL; M93200; AAA60389.1; JOINED.
DR EMBL; M93201; AAA60389.1; JOINED.
DR EMBL; M93202; AAA60389.1; JOINED.
DR EMBL; M93203; AAA60389.1; JOINED.
DR EMBL; M93204; AAA60389.1; JOINED.
DR EMBL; M93205; AAA60389.1; JOINED.
DR EMBL; M93206; AAA60389.1; JOINED.
DR EMBL; M93207; AAA60389.1; JOINED.
DR EMBL; M93208; AAA60389.1; JOINED.
DR EMBL; M93209; AAA60389.1; JOINED.
DR EMBL; M93210; AAA60389.1; JOINED.
DR EMBL; M93211; AAA60389.1; JOINED.
DR EMBL; M93212; AAA60389.1; JOINED.
DR EMBL; M93213; AAA60389.1; JOINED.
DR EMBL; M93214; AAA60389.1; JOINED.
DR EMBL; M93215; AAA60389.1; JOINED.
DR EMBL; M93216; AAA60389.1; JOINED.
DR EMBL; M93217; AAA60389.1; JOINED.
DR EMBL; M93218; AAA60389.1; JOINED.
DR EMBL; M93219; AAA60389.1; JOINED.
DR EMBL; M93220; AAA60389.1; JOINED.
DR PIR; A36563; A36563.
DR PDB; 1EGG; 30-AUG-00.
DR PDB; 1EGI; 30-AUG-00.
DR Genew; HGNC:7228; MRC1.
DR MIM; 153618; -
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005537; F:mannose binding; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0006898; P:receptor mediated endocytosis; TAS.
DR InterPro; IPR002353; Antifreeze1.

DR InterPro; IPR000562; FN Type II.
DR InterPro; IPR001304; Lectin C.
DR InterPro; IPR000772; Ricin B lectin.
DR InterPro; IPR008997; RicinB-like.
DR Pfam; PF00040; fn2; 1.
DR Pfam; PF00059; lectin C; 8.
DR Pfam; PF00652; Ricin B lectin; 2.
DR PRINTS; PR00356; ANTIPEEZELI.
DR PRINTS; PR00013; ANTIPEZELI.
DR ProDom; PD000995; FN Type II; 1.
DR SMART; SM00034; CLECT; 8.
DR SMART; SM00059; FN2; 1.
DR SMART; SM00458; RICIN; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; 6.
DR PROSITE; PS00041; C-TYPE LECTIN 2; 8.
DR PROSITE; PS00023; FIBONECTIN 2; 1.
DR PROSITE; PS00231; RICIN B LECTIN; 1.
KW Receptor; Signal; Calcium-binding; Transmembrane; Repeat;
KW Glycoprotein; Endocytosis; Macrophage; Lectin; Antigen; 3D-structure.
FT SIGNAL 1 18
FT CHAIN 19 1456
FT DOMAIN 19 1383
FT TRANSMEM 1384 1411
FT DOMAIN 1412 1456
FT DOMAIN 22 142
FT DOMAIN 157 212
FT DOMAIN 216 344
FT DOMAIN 360 429
FT DOMAIN 502 621
FT DOMAIN 644 781
FT DOMAIN 893 926
FT DOMAIN 945 1083
FT DOMAIN 1100 1216
FT DOMAIN 1228 1359
FT DISULFID 646 659
FT DISULFID 680 777
FT DISULFID 753 769
FT CARBOHYD 104 134
FT CARBOHYD 344 344
FT CARBOHYD 529 529
FT CARBOHYD 926 926
FT CARBOHYD 930 930
FT CARBOHYD 1160 1160
FT CARBOHYD 1205 1205
FT CARBOHYD 1311 1311
FT TURN 648 649
FT STRAND 651 652
FT TURN 654 655
FT STRAND 658 663
FT STRAND 667 669
FT STRAND 671 671
FT HELIX 673 683
FT TURN 684 684
FT STRAND 686 687
FT HELIX 693 705
FT TURN 706 707
FT TURN 709 710
FT STRAND 712 718
FT TURN 723 724
FT STRAND 727 727
FT TURN 729 730
FT STRAND 733 733
FT TURN 741 742
FT HELIX 746 748
FT STRAND 752 757
FT TURN 758 761
FT STRAND 764 768
FT TURN 769 770
FT STRAND 773 780
FT TURN 781 782
SQ SEQUENCE 1456 AA; 165011 MW; 26455AF3C576A5E3 CRC64;

Query Match

19.5%; Score 81.5; DB 1; Length 1456;

Best Local Similarity 28.8%; Pred. No. 0.39;
Matches 19; Conservative 15; Mismatches 31; Indels 1; Gaps 1;
QY 12 FYIVQEKXNYRESLTHCRIRGMLAMPKDEANTLIADYVAKSGFFRVFVIGVNDLREG 71
Db 960 FGWEERKNQWEAKKACIGFQGNLVISQNEQOALIT-YHMKDSTFFSAWTGLNDVNSEH 1018
QY 72 QYMFTD 77
Db 1019 TFLWTD 1024
RESULT 8
PSPD MOUSE
ID PSPD MOUSE STANDARD; PRT; 374 AA.
AC PS0404;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
GN Pulmonary surfactant-associated protein D precursor (SP-D) (PSP-D).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Lung;
RX MEDLINE=96094460; PubMed=7499882;
RA Motwani M., White R.A., Guo N., Dowler L.L., Tauber A.I., Sastry K.N.;
RT "Mouse surfactant protein-D, cDNA cloning, characterization, and gene
localization to chromosome 14.";
RL J. Immunol. 155:5671-5677(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=99244602; PubMed=10226065;
RA Lawson P.R., Perkins V.C., Holmskov U., Reid K.B.;
RT "Genomic organization of the mouse gene for lung surfactant protein
D.";
RL Am. J. Respir. Cell Mol. Biol. 20:953-963(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Fisher J.H., Sheffelyevich V.V.;
RT "Surfactant protein-D regulates surfactant phospholipid homeostasis in
vivo.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein W.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Contributes to the lung's defense against inhaled
microorganisms. Binds strongly maltose residues and to a lesser
extent other alpha-glucosyl moieties. It could participate in the

CC extracellular reorganization or turnover of pulmonary surfactant.
 CC -!- SUBUNIT: Oligomeric complex of 4 set of homotrimers.
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- MISCELLANEOUS: Pulmonary surfactant consists of 90% lipid and 10%
 CC protein. There are 4 surfactant-associated protein: 2 collagenous,
 CC carbohydrate-binding glycoproteins (SP-A and SP-D) and 2 small
 CC hydrophobic proteins (SP-B and SP-C).
 CC -!- SIMILARITY: Contains 1 collagenous domain.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 CC
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 CC EMBL; L40156; AAA92021.1; -.
 CC EMBL; AF047742; AAD31380.1; -.
 CC EMBL; AF047742; AAD31380.1; JOINED.
 CC EMBL; AF192134; AAF15277.1; -.
 CC EMBL; BC003705; AAH03705.1; -.
 CC HSP; F35247; I808.
 CC MGD; MG1:109515; Sftpd.
 CC InterPro; IPR008160; Collagen.
 CC InterPro; IPR001304; Lectin C.
 CC Pfam; PF01391; Collagen; 3.
 CC Pfam; PF00059; lectin c; 1.
 CC Pfam; PF00034; CLECT; 1.
 CC SMART; SM00034; CLECT; 1.
 CC PROSITE; PS00615; C-TYPE LECTIN_1; 1.
 CC PROSITE; PS00041; C-TYPE LECTIN_2; 1.
 CC Glycoprotein; Calcium; Surface film; Gaseous exchange; Hydroxylation;
 CC Signal; Lectin; Collagen; Repeat; Coiled coil.
 CC SIGNAL 1
 CC BY SIMILARITY.
 CC CHAIN 19
 CC PULMONARY SURFACTANT-ASSOCIATED PROTEIN
 CC D.
 CC DOMAIN 45 221
 CC COLLAGEN-LIKE.
 CC COILED COIL (POTENTIAL).
 CC C-TYPE LECTIN (SHORT FORM).
 CC BY SIMILARITY.
 CC DISULFID 280 372
 CC BY SIMILARITY.
 CC DISULFID 350 364
 CC BY SIMILARITY.
 CC CARBOHYD 89
 CC N-LINKED (GLCNAC...) (POTENTIAL).
 CC SEQUENCE 374 AA; 37688 MW; FE034261263F43E4 CRC64;
 CC
 CC Query Match 19.1%; Score 79.5; DB 1; Length 374;
 CC Best Local Similarity 22.7%; Pred. No. 0.14;
 CC Matches 17; Conservative 14; Mismatches 43; Indels 1; Gaps 1;
 CC
 CC 6 RETEEKYIVQEEKYRESLTHCRIRGGMAMPKDEAMNTLIADYVAKSGFRVFIGVN 65
 CC 257 RSVGDKIFRTADSEKPFEDAQEMCKQAGQLSPRSATENAIIQLITAHN-KAAPLSMT 315
 CC
 CC 66 DLREGQYMTDNTFP 80
 CC 316 DVGTGEKFTYPTGEP 330
 CC
 CC RESULT 9
 CC PSFA HUMAN
 CC ID PSFA_HUMAN
 CC AC P07714;
 CC DT 01-APR-1988 (Rel. 07, Created)
 CC JT 28-APR-1990 (Rel. 14, Last sequence update)
 CC XT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Pulmonary surfactant-associated protein A precursor (SP-A) (PSP-A)
 CC (PSPAP) (Alveolar proteinosis protein) (35 kDa pulmonary surfactant-
 CC associated protein).
 CC (SFTPA1 OR SFTPA OR SFTP1 OR PSAP) AND (SFTPA2 OR SFTPA).
 CC SN Homo sapiens (Human).
 CC XC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CC NCBI_taxid=9606;
 CC

RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86250832; PubMed=3755136;
 RA Floros J., Steinbrink R., Jacobs K., Phelps D., Kriz R., Recny M.,
 RA Soltzman L., Jones S., Tausch H.W., Frank H.A., Fritsch E.F.,
 "Isolation and characterization of cDNA clones for the 35-kDa
 FT pulmonary surfactant-associated protein.",
 RL J. Biol. Chem. 261:9029-9033 (1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86014366; PubMed=2995821;
 RA White R.T., Damm D., Miller J., Spratt K., Schilling J., Hawgood S.,
 RA Benson B., Cordell B.;
 FT "Isolation and characterization of the human pulmonary surfactant
 RT apoprotein gene.",
 RL Nature 317:361-363 (1985).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92198680; PubMed=1372511;
 RA Katyal S.L., Singh G., Locker J.L.;
 FT "Characterization of a second human pulmonary surfactant-associated
 RT protein SP-A gene.",
 RL Am. J. Respir. Cell Mol. Biol. 6:446-452 (1992).
 CC -!- FUNCTION: In presence of calcium ions, PSAP binds to surfactant
 CC phospholipids and contributes to lower the surface tension at the
 CC air-liquid interface in the alveoli of the mammalian lung and is
 CC essential for normal respiration.
 CC -!- SUBUNIT: Oligomeric complex of 6 set of homotrimers.
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- MISCELLANEOUS: Pulmonary surfactant consists of 90% lipid and 10%
 CC protein. There are 4 surfactant-associated protein: 2 collagenous,
 CC carbohydrate-binding glycoproteins (SP-A and SP-D) and 2 small
 CC hydrophobic proteins (SP-B and SP-C).
 CC -!- SIMILARITY: Contains 1 collagenous domain.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 CC
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 CC
 CC EMBL; M13686; AAA60211.1; -.
 CC EMBL; K03475; AAA36520.1; -.
 CC EMBL; M30838; AAA36510.1; -.
 CC EMBL; M68519; AAA60319.1; -.
 CC PIR; A25720; LNHUP6.
 CC HSP; P22897; LEGG.
 CC Genew; HGNC:10798; SFTPA1.
 CC Genew; HGNC:10799; SFTPA2.
 CC MIN; 178630; -.
 CC MIN; 178642; -.
 CC GO; GO:0005319; Fil lipid transporter activity; TAS.
 CC InterPro; IPR008160; Collagen.
 CC InterPro; IPR001304; Lectin C.
 CC Pfam; PF01391; Collagen; 2.
 CC Pfam; PF00059; lectin c; 1.
 CC SMART; SM00034; CLECT; 1.
 CC PROSITE; PS00615; C-TYPE LECTIN_1; 1.
 CC PROSITE; PS00041; C-TYPE LECTIN_2; 1.
 CC Glycoprotein; Calcium; Surface film; Gaseous exchange; Hydroxylation;
 CC Signal; Lectin; Collagen; Repeat; Polymorphism.
 CC SIGNAL 1
 CC CHAIN 21 248
 CC PULMONARY SURFACTANT-ASSOCIATED PROTEIN
 CC A.
 CC DOMAIN 28 100
 CC COLLAGEN-LIKE.
 CC C-TYPE LECTIN (SHORT FORM).
 CC BY SIMILARITY.
 CC DISULFID 155 246
 CC BY SIMILARITY.
 CC DISULFID 224 238
 CC BY SIMILARITY.
 CC CARBOHYD 207 207
 CC N-LINKED (GLCNAC...) (PROBABLE).
 CC VARIANT 9
 CC N -> T.

CC RX TISSUE=Breast tumor;
CC RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Hopkins S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Moore I., Max S.I., Wang J.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richardson S., Worley D.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RN SEQUENCE OF 114-328 FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Embryo;
RX MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Oatono N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Fagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Giasi C., Godzik A., Gough J.,
RA Grimmond S., Gusincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasaki Y., Kedzierski R.M., King B.D.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Seiple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Vercarlo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda I.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
CC -!- FUNCTION: Stimulates the proliferation and differentiation of
CC hematopoietic precursor cells from various lineages, including
CC erythrocytes, lymphocytes, granulocytes and macrophages. Acts
CC synergistically with other cytokines, including IL-3, G-CSF, GM-CSF
CC and Flt3 ligand. Suppresses SCF-stimulated erythrocyte
CC proliferation (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and secreted (By
CC similarity).
CC -!- PTM: O-glycosylated. Probably sulfated on the O-glycans (By
CC similarity).
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
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CC -----
CC EMBL: AB009245; BAA32405.1; -
CC EMBL: EC002001; AAH02001.3; -
CC EMBL: AK042963; BAC31421.1; -
CC EMBL: AK003813; BAB23010.1; -
CC HSSP: P05452; 1HTN.
CC MGD: MGI:1298219; Scgf.
CC GO: GO:0005576; C:extracellular; ISS.
CC GO: GO:0008083; P:growth factor activity; ISS.
CC GO: GO:0005529; P:sugar binding; NAS.
CC GO: GO:0008284; P:positive regulation of cell proliferation; ISS.
CC InterPro: IPR001304; LECTIN_C.
CC Pfam: PF00059; LECTIN_C.1.
CC SMART: SM00034; CLECT.1.
CC PROSITE: PS00615; C_TYPE_LECTIN_1; 1.
CC PROSITE: PS00041; C_TYPE_LECTIN_2; 1.
CC Growth factor; Glycoprotein; Lectin; Signal.
CC SIGNAL 1 21 BY SIMILARITY.
CC FT CHAIN 22 328 STEM CELL GROWTH FACTOR.
CC FT DOMAIN 188 325 C-TYPE LECTIN.
CC FT CONFLICT 114 117 TYIL -> FFTV (IN REF. 3).
CC SQ SEQUENCE 328 AA; 36451 MW; 309C17A861EE135C CRC64;
Query Match 18.7%; Score 78; DB 1; Length 328;
Best Local Similarity 27.3%; Pred. No. 0.18; 33; Indels 4; Gaps 3;
Matches 21; Conservative 19; Mismatches 33;
QY 2 IAGIRETEEFYIVQEKYRESLTHCRIRGMLAMPKDEAANTLIADYV--AKSGF-F 58
DB 183 LKGLR-LGHKFLLSRDFETQAAQAQRCARGSLAQPADRCQDALSRYLAALPYNW 241
QY 59 RVFIGNVDLREGOYMF 75
DB 242 PVWGVHDSRSEGLYLF 258
RESULT 12
SCGF RAT
ID SCGF RAT STANDARD; PRT; 328 AA.
AC OS8201;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Stem cell growth factor precursor (Lymphocyte secreted C-type
DE lectin).
GN SCGF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Bone;
RX MEDLINE=98381038; PubMed=9705843;
RA Mio H., Kagami N., Yokokawa S., Kawai H., Nakagawa S., Takeuchi K.,
RA Sekine S., Hiraoka A.;
RT "Isolation and characterization of a cDNA for human, mouse, and rat
RT full-length stem cell growth factor, a new member of C-type lectin
RT superfamily";
RL Biochem. Biophys. Res. Commun. 249:124-130 (1998).
CC -!- FUNCTION: Stimulates the proliferation and differentiation of
CC hematopoietic precursor cells from various lineages, including
CC erythrocytes, lymphocytes, granulocytes and macrophages. Acts
CC synergistically with other cytokines, including IL-3, G-CSF, GM-CSF
CC and Flt3 ligand. Suppresses SCF-stimulated erythrocyte
CC proliferation (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and secreted (By
CC similarity).
CC -!- PTM: O-glycosylated. Probably sulfated on the O-glycans (By
CC similarity).
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----

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DR EMBL; AB009246; BAA32406.1; -;
DR HSP; P05452; 1HTN.
DR GO; GO:0005576; C:extracellular; IDA.
DR GO; GO:0008083; F:growth factor activity; IDA.
DR GO; GO:0005529; F:sugar binding; NAS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR InterPro; IPR001304; LECTIN_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; 1.
DR PROSITE; PS00041; C TYPE LECTIN 2; 1.
KW Growth factor; Glycoprotein; Lectin; Signal.
FT SIGNAL 1 21
FT CHAIN 22 328
FT DOMAIN 188 325
FT C-TYPE LECTIN.
SQ SEQUENCE 328 AA; 36387 MW; C115188AC23D6257 CRC64;

Query Match 18.7%; Score 78; DB 1; Length 328;
Best Local Similarity 27.3%; Pred. No. 0.18; Indels 4; Gaps 3;
Matches 21; Conservative 19; Mismatches 33; Indels 4; Gaps 3;
QY 2 IAGIRETEKFFYIVQEKYKNSLTHCRIRGGMAMPKDEAANTLIADYV--AKSGP-F 58
Db 183 LKGLR-LGHKCFLLSRPETQAAQARKGGSGLAQPADRQMDALSRYLAALAPYNN 241
QY 59 RVFIGVNDLEREGQMF 75
Db 242 PVNLGVHRRSEGLYLF 258

RESULT 13
KUCR RAT
ID KUCR RAT STANDARD; PRT; 550 AA.
AC P10716;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-type lectin 13 (Kupffer cell receptor).
GN CLEGF13 OR KCLR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 83-104.
RX MEDLINE=88227939; PubMed=2836387;
RA Hoyle G.W., Hill R.L.;
RT "Molecular cloning and sequencing of a cDNA for a carbohydrate
RT binding receptor unique to rat Kupffer cells.";
RL J. Biol. Chem. 263:7487-7492(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91107689; PubMed=1846367;
RA Hoyle G.W., Hill R.L.;
RT "Structure of the gene for a carbohydrate-binding receptor unique to
RT rat Kupffer cells.";
RL J. Biol. Chem. 266:1850-1857(1991).
CC -!- FUNCTION: Receptor with an affinity for galactose and fucose.
CC Could be involved in endocytosis.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- TISSUE SPECIFICITY: Kupffer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

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DR EMBL; J03734; AAA41472.1; -;
DR EMBL; M55532; AAA40892.1; -;
DR PIR; A38674; A28166.
DR HSP; P20693; IHLJ.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; LECTIN_C.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; 1.
DR PROSITE; PS00041; C TYPE LECTIN 2; 1.
KW Receptor; Transmembrane; Glycoprotein; Lectin; Signal-anchor;
KW Endocytosis.
FT DOMAIN 1 42
FT TRANSMEM 43 69
FT CYTOPLASMIC (POTENTIAL).
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 70 550
FT DOMAIN 438 538
FT DISULFID 440 536
FT DISULFID 516 528
FT CARBOHYD 87 87
FT CARBOHYD 93 93
FT CARBOHYD 115 115
FT CARBOHYD 132 132
FT CARBOHYD 209 209
FT CARBOHYD 255 255
SQ SEQUENCE 550 AA; 61104 MW; 9358A6CF4C306270 CRC64;

Query Match 18.8%; Score 77.5; DB 1; Length 550;
Best Local Similarity 27.1%; Pred. No. 0.36; Indels 3; Gaps 1;
Matches 19; Conservative 14; Mismatches 34; Indels 3; Gaps 1;
QY 11 KFYIVQEEKYKNSLTHCRIRGGMAMPKDEAANTLIADYVAKSGFPRFVIGVNDLERE 70
Db 422 KFYFSDKKSWEAENFCVSGAHLASVTSOEQAFL--VQITNAVDFHIGLTDQGT 478
QY 71 GQYMFDTNTP 80
Db 479 GNRWVDGTP 488

RESULT 14
CONG_BOVIN
ID CONG_BOVIN STANDARD; PRT; 371 AA.
AC P23805; O97748;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Conglutinin precursor.
GN CGN1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93213261; PubMed=8460993;
RA Suzuki Y., Yin J., Makino M., Kurimura T., Wakamiya N.;
RT "Cloning and sequencing of a cDNA coding for bovine conglutinin.";
RL Biochem. Biophys. Res. Commun. 191:335-342(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93277452; PubMed=7684896;
RA Lu J., Laursen S.B., Thiel S., Jensenius J.C., Reid B.M.;
RT "The cDNA cloning of conglutinin and identification of liver as a
RT primary site of synthesis of conglutinin in members of the Bovidae.";

Biochem. J. 292:157-162(1993).
 [3]
 SEQUENCE FROM N.A.
 TISSUE=Liver;
 RX MEDLINE=94215917; PubMed=8163202;
 RA Liou L.S., Sastry R., Harthorn K.L., Lee Y.M., Okarma T.B.,
 Tauber A.I., Sastry K.N.,
 RT "Bovine conglutinin (BC) mRNA expressed in liver: cloning and
 RT characterization of the BC cDNA reveals strong homology to surfactant
 RT protein-D";
 RL Gene 141:277-281(1994).
 [4]
 SEQUENCE FROM N.A.
 TISSUE=Liver;
 RX MEDLINE=94267222; PubMed=8207234;
 RA Liou L.S., Sastry R., Harthorn K.L., Lee Y.M., Okarma T.B.,
 Tauber A.I., Sastry K.N.,
 RT "Bovine conglutinin gene exon structure reveals its evolutionary
 RT relationship to surfactant protein-D";
 RL J. Immunol. 153:173-180(1994).
 [5]
 SEQUENCE FROM N.A.
 TISSUE=Liver;
 RX MEDLINE=94128104; PubMed=8297370;
 RA Kawasaki N., Itoh N., Kawasaki T.,
 RT "Gene organization and 5'-flanking region sequence of conglutinin: a
 RT C-type mammalian lectin containing a collagen-like domain";
 RL Biochem. Biophys. Res. Commun. 198:597-604(1994).
 [6]
 SEQUENCE OF 21-371.
 RX MEDLINE=91131556; PubMed=1993651;
 RA Lee Y.-W., Leiby K.R., Allar J., Paris K., Lerch B., Okarma T.B.,
 RT "Primary structure of bovine conglutinin, a member of the C-type
 RT animal lectin family";
 RL J. Biol. Chem. 266:2715-2723(1991).
 [7]
 PRELIMINARY SEQUENCE OF 21-52.
 RX MEDLINE=87184551; PubMed=3566740;
 RA Young N.M., Jeon M.A.;
 RT "The carbohydrate specificity of conglutinin and its homology to
 RT proteins in the hepatic lectin family";
 RL Biochem. Biophys. Res. Commun. 143:645-651(1987).
 CC -!- FUNCTION: Calcium-dependent lectin-like protein which binds to a
 CC yeast cell wall extract and immune complexes through the
 CC complement component (C3bi). It is capable of binding nonreducing
 CC terminal N-acetylglucosamine, mannose, and fucose residues.
 CC -!- SUBUNIT: Oligomeric complex of 4 set of homotrimers.
 CC -!- SIMILARITY: Contains 1 collagenous domain.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 CC -----
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 CC -----
 RX EMBL; D14085; BAA03170.1; -
 RX EMBL; X71774; CAA50665.1; -
 RX EMBL; L18871; AAA20126.1; -
 RX EMBL; U06860; AAB60624.1; -
 RX EMBL; U06854; AAB60624.1; JOINED.
 RX EMBL; U06855; AAB60624.1; JOINED.
 RX EMBL; U06856; AAB60624.1; JOINED.
 RX EMBL; U06857; AAB60624.1; JOINED.
 RX EMBL; U06858; AAB60624.1; JOINED.
 RX EMBL; U06859; AAB60624.1; JOINED.
 RX EMBL; D25302; BAA04983.2; -
 RX EMBL; D25296; BAA04983.2; JOINED.
 RX EMBL; D25297; BAA04983.2; JOINED.
 RX EMBL; D25298; BAA04983.2; JOINED.
 RX EMBL; D25299; BAA04983.2; JOINED.

DR EMBL; D25300; BAA04983.2; JOINED.
 DR EMBL; D25301; BAA04983.2; JOINED.
 DR PIR; I45878; I45878.
 DR PIR; JN0450; JN0450.
 DR HSSP; P35247; 1808.
 DR InterPro; IPR008161; Clg_helix.
 DR InterPro; IPR008160; Collagen.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF01391; Collagen; 3.
 DR Pfam; PF00059; Lectin_C; 1.
 DR ProDom; PD000007; Clg_helix; 1.
 DR SMART; SMO0034; CLEC; 1.
 DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.
 DR PROSITE; PS50041; C-TYPE LECTIN 2; 1.
 KW Lectin; Hydroxylation; Glycoprotein; Mannose-binding; Membrane;
 KW Collagen; Repeat; Calcium; Signal.
 FT SIGNAL 1 20 CONGLUTININ.
 FT CHAIN 21 371 COLLAGEN-LIKE.
 FT DOMAIN 46 216 C-TYPE LECTIN (SHORT FORM).
 FT DOMAIN 273 371 HYDROXYLATION.
 FT MOD_RES 63 63 HYDROXYLATION.
 FT MOD_RES 87 87 HYDROXYLATION.
 FT MOD_RES 99 99 HYDROXYLATION.
 FT MOD_RES 135 135 HYDROXYLATION.
 FT MOD_RES 141 141 HYDROXYLATION.
 FT MOD_RES 159 159 HYDROXYLATION.
 FT MOD_RES 162 162 HYDROXYLATION.
 FT MOD_RES 198 198 HYDROXYLATION.
 FT SITE 201 203 CELL ATTACHMENT SITE (POTENTIAL).
 FT DISULFID 275 369 BY SIMILARITY.
 FT CARBOHYD 337 337 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 173 173 R -> H (IN REF. 2 AND 3).
 FT CONFLICT 210 210 K -> S (IN REF. 6).
 FT CONFLICT 218 218 V -> A (IN REF. 2).
 FT CONFLICT 272 272 E -> V (IN REF. 2).
 SQ SEQUENCE 371 AA; 37594 MW; 867EB41992544B1F CRC64;
 Query Match 18.3%; Score 76.5; DB 1; Length 371;
 Best Local Similarity 25.8%; Pred. No. 0.3;
 Matches 17; Conservative 15; Mismatches 33; Indels 1; Gaps 1;
 QY 10 EKYYIVQEEKYRESLTHCRTRGGGLAMPKDEANTLIADYVAKSGFRVFIGVNDLER 69
 DB 256 EKIFTAGAVKSYSDAEQLCREAKQOLASPRSSAENEAVTQMV-PAQKNAYLSMNDIST 314
 QY 70 EGQYMF 75
 DB 315 EGRFTY 320
 RESULT 15
 KUCR MOUSE
 ID KUCR MOUSE STANDARD; PRT; 548 AA.
 AC P70194;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-type lectin 13 (Kupffer cell receptor).
 GN CLECSF13 OR KCLR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RA Takezawa R., Wagatsuma H., Nomoto C., Watanabe Y., Akaike T.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Liver;
 RX MEDLINE=22388257; PubMed=12477932;

[illegible]

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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:03:01 ; Search time 21.1454 Seconds
(without alignments)
363.925 Million cell updates/sec

Title: US-09-600-932-2_COPY_148_227

Perfect score: 417

Sequence: 1 VIAGIRETEKFFYIVQBEK.....FIGVNDLEREGQYMTDNT 80

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR 78:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	405	97.1	277	2 JC7903	collectin liver 1
2	91	21.8	166	1 A37289	tetranectin homolo
3	89.5	21.2	404	2 A45274	HIV gp120-binding
4	83.5	20.0	369	2 S38603	surfactant protein
5	82.5	19.8	1326	2 B36395	secretory phosphol
6	82.5	19.8	1465	2 A56395	secretory phosphol
7	82	19.7	202	1 TTHUN	tetranectin precu
8	82	19.7	321	2 T19259	hypothetical prote
9	81.5	19.5	301	2 A53570	collectin-43 - bov
10	81.5	19.5	1456	1 A36563	mannose receptor p
11	78.5	18.8	248	1 LNHUP5	pulmonary surfacta
12	78.5	18.8	248	1 LNHUP6	pulmonary surfacta
13	78.5	18.8	248	1 LNHUP1	pulmonary surfacta
14	78.5	18.8	248	2 I51921	pulmonary surfacta
15	78	18.7	202	2 JC4031	tetranectin precu
16	78	18.7	321	2 T36152	hypothetical prote
17	77.5	18.6	550	2 A28166	Kupffer cell recep
18	76.5	18.3	371	1 JN0450	conglutinin precu
19	76.5	18.3	371	2 I45878	conglutinin - bovi
20	74.5	17.9	1479	2 T42710	mannose receptor,
21	74	17.7	238	1 LNR7WA	mannose-binding le
22	73.5	17.6	155	2 S78774	perlucin - Haloti
23	73	17.5	321	2 T36153	hypothetical prote
24	71.5	17.1	374	1 A42046	surfactant protein
25	71.5	17.1	1450	2 T30273	hypothetical prote
26	71.5	17.1	1487	2 S48719	phospholipase-A(2)
27	70.5	16.9	331	1 S34198	IgE Fc receptor II
28	70.5	16.9	309	1 LNM5ER	IgE Fc receptor, I
29	70.5	16.9	1458	1 A49707	phospholipase A2 r

30 69.5 16.7 162 1 LNRC1
31 69.5 16.7 162 1 LNRC3
32 69.5 16.7 188 2 I59421
33 69.5 16.7 317 2 AB0281
34 69.5 16.7 1463 2 A53210
35 69 16.5 107 2 F83522
36 69 16.5 330 2 T46256
37 69 16.5 828 1 D39142
38 68.5 16.4 2890 2 F64669
39 68 16.3 705 2 T18547
40 68 16.3 1294 2 T18546
41 67.5 16.2 314 2 AC0683
42 67 16.1 237 2 JC7608
43 66.5 15.9 375 1 A45225
44 66.5 15.9 872 2 S55940
45 66.5 15.9 1455 1 A48925

ALIGNMENTS

RESULT 1

JC7903
collectin liver 1 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 03-Feb-2003 #sequence_revision 03-Feb-2003 #text_change 31-Mar-2003
C:Accession: JC7903
R:Kawai, T.; Suzuki, Y.; Eda, S.; Kase, T.; Ohtani, K.; Sakai, Y.; Keshi, H.; Fukuh, A
Biosci. Biotechnol. Biochem. 66, 2134-2145, 2002.
A:Title: Molecular cloning of mouse collectin liver 1.
A:Reference number: JC7903; MUID:22333927; PMID:12450124
A:Accession: JC7903
A:Molecule type: mRNA
A:Residues: 1-277 <RAW>
A:Cross-references: DDBJ:AB016429
A:Experimental source: liver
C:Comment: This protein is a highly conserved cytosolic protein and belongs to a vertebrate development.
C:Genetics:
A:Gene: C11
A:Map position: 15

Query Match 97.1%; Score 405; DB 2; Length 277;
Best Local Similarity 96.2%; Pred. No. 8.2e-40;
Matches 77; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 VIAGIRETEKFFYIVQBEKKNYRESLTHCRIRGMLAMPKDEANNTLIADYVAKSGFFRV 60
DB 148 VIAGIRETEKFFYIVQBEKKNYRESLTHCRIRGMLAMPKDEYVNTLIADYVAKSGFFRV 207
QY 61 FIGVNDLEREGQYMTDNT 80
DB 208 FIGVNDLEREGQYMTDNT 227

RESULT 2

A37289
tetranectin homolog - reef shark
C:Species: Carcharhinus springeri (reef shark)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A37289; A37287
R:Neame, P.J.; Young, C.N.; Treep, J.T.
Protein Sci. 1, 161-168, 1992.
A:Title: Primary structure of a protein isolated from reef shark Carcharhinus springeri
A:Reference number: A37289; MUID:93284081; PMID:1304877
A:Accession: A37289
A:Molecule type: protein
A:Residues: 1-166 <NE2>
C:Superfamily: tetranectin; C-type lectin homology
C:Keywords: cartilage
F:37-160/Domain: C-type lectin homology <LCH>
F:37-47,64-160,136-152/Disulfide bonds: #status predicted

Query Match 21.8%; Score 91; DB 1; Length 166;
Best Local Similarity 28.8%; Pred. No. 0.0031;
Matches 21; Conservative 15; Mismatches 35; Indels 2; Gaps 1;

QY 10 EKFFVYVVEKNYRESLTHCRIRGMLAMPKDEAANTLIADYVAKS--GFPRVFIGVNDL 67
DB 45 KCYLASGSKSYHAANEDCTAAGTSLIPRSSDEGNSLSYAKSLVGVARDFWIGVNDM 104
QY 68 EREGQYMTDNT 80
DB 105 TTEGRFVDVNGLP 117

RESULT 3
HIV gp120-binding C-type lectin - human
C/Species: Homo sapiens (man)
C/Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-1995
C/Accession: A46274
R/Curtis, B.M.; Scharnowske, S.; Watson, A.J.
Proc. Natl. Acad. Sci. U.S.A. 89, 8356-8360, 1992
A/Title: Sequence and expression of a membrane-associated C-type lectin that exhibits CD
A/Reference number: A46274; MUID:92390446; PMID:11518869
A/Accession: A46274
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-404 <CUR>
A/Experimental source: placenta
A/Note: sequence extracted from NCBI backbone (NCBIN:113134, NCBIIP:113135)
C/Superfamily: C-type lectin homology
F:256-377/Domain: C-type lectin homology <LCH>

Query Match 21.2%; Score 88.5; DB 2; Length 404;
Best Local Similarity 25.0%; Pred. No. 0.018;
Matches 17; Conservative 20; Mismatches 30; Indels 1; Gaps 1;

QY 13 YVVEKNYRESLTHCRIRGMLAMPKDEAANTLIADYVAKSGFPRVFIGVNDLREQ 72
DB 268 YFMSQNSQNHDSITACKVEGAQLWIKSAEQNFLOQSSRSNRP-TWVGUSDNLQEGT 326
QY 73 YNFTDNT 80
DB 327 MQVVDGSP 334

RESULT 4
S33603
surfactant protein D - bovine
C/Species: Bos primigenius taurus (cattle)
C/Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
C/Accession: S33603
R/Lim, B.D.; Lu, J.; Reid, K.B.M.
Immunology 78, 159-165, 1993
A/Title: Structural similarity between bovine conglutinin and bovine lung surfactant pro
A/Reference number: S33603; MUID:93170856; PMID:8436402
A/Accession: S33603
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-369 <LIM>
C/Superfamily: pulmonary surfactant protein D; C-type lectin homology
F:248-367/Domain: C-type lectin homology <LCH>

Query Match 20.0%; Score 83.5; DB 2; Length 369;
Best Local Similarity 25.3%; Pred. No. 0.062;
Matches 19; Conservative 16; Mismatches 39; Indels 1; Gaps 1;

QY 6 RTESEKFFVVOEKNYRESLTHCRIRGMLAMPKDEAANTLIADYVAKSGFPRVFIGV 65
DB 252 RSVGKIFKTVGSEKTFQDAQICTQAGGQLPSRSGAENEALQ-LATAQNKAFPLMS 310
QY 66 DLREGQYMTDNT 80
DB 311 DTRKEGTFTYGTGP 325

RESULT 5

B56395
secretory phospholipase A2 receptor precursor, soluble form - human
C/Species: Homo sapiens (man)
C/Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C/Accession: B56395
R/Ancian, P.; Lambeau, G.; Mattei, M.G.; Lazdunski, M.
J. Biol. Chem. 270, 8963-8970, 1995
A/Title: The human 180-kDa receptor for secretory phospholipases A-2. Molecular cloning,
A/Reference number: A56395; MUID:95238395; PMID:7721806
A/Accession: B56395
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-1326 <ANC>
A/Cross-references: GB:U17034; NID:G862376; PIDN:AAC50163.1; PID:G862377
C/Genetics:
A/Map position: 2q23-q24
C/Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II re
C/Keywords: alternative splicing; extracellular protein
F:180-221/Domain: fibronectin type II repeat homology <2F1>
F:380-503/Domain: C-type lectin homology <LCH>

Query Match 19.8%; Score 82.5; DB 2; Length 1326;

Best Local Similarity 26.7%; Pred. No. 0.38;

Matches 16; Conservative 19; Mismatches 24; Indels 1; Gaps 1;

QY 21 NYRESLTHCRIRGMLAMPKDEAANTLIADYVAKSGFPRVFIGVNDLREGQYMTDNT 80

DB 254 SWSEAHSSCOMQGGTLLSTDETEENFIREHMS-SKTVEVWVGLNQLDDEAGWQSDGTP 312

RESULT 6

A56395
secretory phospholipase A2 receptor precursor, transmembrane form - human
C/Species: Homo sapiens (man)
C/Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 20-Aug-1999
C/Accession: A56395
R/Ancian, P.; Lambeau, G.; Mattei, M.G.; Lazdunski, M.
J. Biol. Chem. 270, 8963-8970, 1995
A/Title: The human 180-kDa receptor for secretory phospholipases A-2. Molecular cloning,
A/Reference number: A56395; MUID:95238395; PMID:7721806
A/Accession: A56395
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-1465 <ANC>
A/Cross-references: GB:U17033; NID:G862374; PIDN:AAA70110.1; PID:G862375
C/Genetics:
A/Map position: 2q23-q24
C/Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II re
C/Keywords: alternative splicing; transmembrane protein
F:180-221/Domain: fibronectin type II repeat homology <2F1>
F:380-503/Domain: C-type lectin homology <LCH>

Query Match 19.8%; Score 82.5; DB 2; Length 1465;

Best Local Similarity 26.7%; Pred. No. 0.43;

Matches 16; Conservative 19; Mismatches 24; Indels 1; Gaps 1;

QY 21 NYRESLTHCRIRGMLAMPKDEAANTLIADYVAKSGFPRVFIGVNDLREGQYMTDNT 80

DB 254 SWSEAHSSCOMQGGTLLSTDETEENFIREHMS-SKTVEVWVGLNQLDDEAGWQSDGTP 312

RESULT 7

THUN
tetranectin precursor [validated] - human
N/Alternate names: plasminogen-kringle 4 binding protein
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1992 #sequence_revision 03-Aug-1995 #text_change 08-Dec-2000
A/Accession: S24126; A56835; A29747; I38359; S19865
R/Berglund, L.; Petersen, T.E.
FEBS Lett. 309, 15-19, 1992

A;Title: The gene structure of tetranectin, a plasminogen binding protein.
A;Reference number: S24126; MUID:92380263; PMID:1511740
A;Accession: S24126
A;Molecule type: DNA
A;Residues: 1-202 <BER>
A;Cross-references: EMBL:X70911
R;Wewer, U.M.; Albrechtsen, R.
Lab. Invest. 67, 253-262, 1992
A;Title: Tetranectin, a plasminogen kringle 4-binding protein. Cloning and gene expression.
A;Reference number: A56835; MUID:92365345; PMID:1354271
A;Accession: A56835
A;Molecule type: mRNA
A;Residues: 1-202 <EW>
A;Cross-references: EMBL:X64559; NID:G37408; PIDN:CAA45860.1; PID:G37409
R;Puhlendorff, J.; Clemmensen, I.; Magnusson, S.
Biochemistry 26, 6757-6764, 1987
A;Title: Primary structure of tetranectin, a plasminogen kringle 4 binding plasma protein.
A;Reference number: A29747; MUID:88107595; PMID:3427041
A;Accession: A29747
A;Molecule type: protein
A;Residues: 22-105, 'G', 107-202 <FUH>
A;Experimental source: plasma
A;Note: 55-Ser and 58-Met were also found
C;Genetics:
A;Gene: GDB:TNA
A;Cross-references: GDB:135032; OMIM:187520
A;Map position: 3p22-3p21.3
A;Introns: 37/1; 70/1
C;Complex: homotetramer
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: Glycoprotein; plasma; tetramer
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-202/Product: tetranectin #status experimental <MAT>
F;71-197/Domain: C-type lectin homology <LCH>
F;25/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;1-81, 98-197, 173-189/Disulfide bonds: #status experimental

Query Match 19.7%; Score 82; DB 1; Length 202;
Best Local Similarity 25.8%; Pred. No. 0.045;
Matches 17; Conservative 18; Mismatches 29; Indels 2; Gaps 1;
Mates 17; Conservative 18; Mismatches 29; Indels 2; Gaps 1;
QY 11 KFYVQEKYKRESLTHCRIRGGMAMPKDEAANTLIADYVAKS--GPRVFIGVNDLE 68
DB 80 KCFLAFTQTKTFHEASEDCISRGTLSTPQTGSENDALYLRQSVGNRAEIIWGLNDMA 139
QY 69 REGQYM 74
DB 140 AEGTWV 145

RESULT 8
T19259
hypothetical protein C14A6.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T19259
R;Mortimore, B.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19038
A;Accession: T19259
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-321 <WIL>
A;Cross-references: EMBL:Z81470; PIDN:CA803881.1; GSPDB:GN00023; CESP:C14A6.1
A;Experimental source: clone C14A6
C;Genetics:
A;Gene: CESP:C14A6.1
A;Map position: 5
A;Introns: 32/2; 164/1; 232/1

Query Match 19.7%; Score 82; DB 2; Length 321;
Best Local Similarity 30.4%; Pred. No. 0.079;
Matches 17; Conservative 18; Mismatches 29; Indels 2; Gaps 1;
Mates 17; Conservative 18; Mismatches 29; Indels 2; Gaps 1;
QY 11 KFYVQEKYKRESLTHCRIRGGMAMPKDEAANTLIADYVAKS--GPRVFIGVNDLE 68
DB 80 KCFLAFTQTKTFHEASEDCISRGTLSTPQTGSENDALYLRQSVGNRAEIIWGLNDMA 139
QY 69 REGQYM 74
DB 140 AEGTWV 145

RESULT 9
A53570
collectin-43 - bovine
N;Alternate names: lectin CL-43
C;Species: Bos primigenius taurus (cattle)
C;Date: 12-Apr-1995 #sequence_revision 23-Feb-1996 #text_change 17-Mar-1999
A;Accession: A53570; A46689
R;Lim, B.L.; Willis, A.C.; Reid, K.B.M.; Lu, J.; Laursen, S.B.; Jensenius, J.C.; Holmsk
J. Biol. Chem. 269, 11820-11824, 1994
A;Title: Primary structure of bovine collectin-43 (CL-43). Comparison with conglutinin.
A;Reference number: A53570; MUID:94216283; PMID:8163480
A;Accession: A53570
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-301 <LIM>
A;Cross-references: GB:X75912
R;Holmskov, U.; Teisner, B.; Willis, A.C.; Reid, K.B.; Jensenius, J.C.
J. Biol. Chem. 268, 10120-10125, 1993
A;Title: Purification and characterization of a bovine serum lectin (CL-43) with structu
A;Reference number: A46689; MUID:93252891; PMID:8486682
A;Accession: A46689
A;Molecule type: protein
A;Residues: 1-27 <HOL>
A;Experimental source: serum
A;Note: sequence extracted from NCBI backbone (NCBI:131234)
C;Superfamily: pulmonary surfactant protein D; C-type lectin homology
C;Keywords: lectin
F;177-299/Domain: C-type lectin homology <LCH>

Query Match 19.5%; Score 81.5; DB 2; Length 301;
Best Local Similarity 28.4%; Pred. No. 0.083;
Matches 19; Conservative 15; Mismatches 30; Indels 3; Gaps 2;
Mates 19; Conservative 15; Mismatches 30; Indels 3; Gaps 2;
QY 10 EKFYVQEKYKRESLTHCRIRGGMAMPKDEAANTLIADYVAKS--GPRVFIGVNDLE 68
DB 185 EKIFPKTAGVKSYSDAEQLCREAKGQLASPRSSAENEAVTLVRANK--HAYLSMNDIS 242
QY 69 REGQYM 75
DB 243 KEGFTY 249

RESULT 10
A36563
mannose receptor precursor - human
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
A;Accession: A36563; A60926; A44255; B44255; C44255; D44255; F44255; G44255; H4
R;Taylor, M.E.; Conary, J.T.; Lennartz, M.R.; Stahl, P.D.; Drickamer, K.
J. Biol. Chem. 265, 12156-12162, 1990
A;Title: Primary structure of the mannose receptor contains multiple motifs resembling
A;Reference number: A36563; MUID:90324192; PMID:2373685
A;Accession: A36563
A;Molecule type: mRNA
A;Residues: 1-1456 <RAY>
A;Cross-references: GB:J05550; NID:gl88675; PIDN:AAA59868.1; PID:gl88676
A;Note: parts of this sequence, including the amino end of the mature protein, were conf
R;Ezekowitz, R.A.B.; Sastry, K.; Bailly, P.; Warner, A.
J. Exp. Med. 172, 1785-1794, 1990
A;Title: Molecular characterization of the human macrophage mannose receptor: demonstrat
A;Reference number: A60926; MUID:91079783; PMID:2258707
A;Accession: A60926

A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1333, T, 1335-1456 <EZE>
A:Cross-references: GB:X55635
A>Note: translation of the nucleotide sequence is incomplete
R>Note: in the authors' translation additional residues Pro-Glu-Ile are shown after 497-
R:Kim, S.J.; Ruiz, N.; Bezouska, K.; Drickamer, K.
Genomics 14, 721-727, 1992
A:Title: Organization of the gene encoding the human macrophage mannose receptor (MRC1).
A:Reference number: A44255; MUID:93052405; PMID:1294118
A:Accession: A44255
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: DNA
A:Residues: 155-233, 'KSAL', 238-283;346-428;492-569;631-714,716-719;783-820,'N',822-865;
A>Note: sequence extracted from NCBI backbone (NCBIP:118415, NCBIP:118421, NCBIP:118428,
C:Genetics:
A:Gene: GDB:MRC1
A:Cross-references: GDB:133759; OMIM:153618
A:Map position: 10p13-10p13
C:Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II re
C:Keywords: duplication; lectin; tandem repeat; transmembrane protein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:168-209/Domain: fibronectin type II repeat homology <2F1>
F:223-340/Domain: C-type lectin homology <LCH1>
F:362-486/Domain: C-type lectin homology <LCH2>
F:945-1079/Domain: C-type lectin homology <LCH3>

Query Match 19.5%; Score 81.5; DB 1; Length 1456;
Best Local Similarity 28.8%; Pred. No. 0.56;
Matches 19; Conservative 15; Mismatches 31; Indels 1; Gaps 1;

QY 12 FYIIVQEKYRESLTHCRIGGMLAMPKDEAANTLIADYVAKSGFRVPIGVNDLERG 71
DB 960 FGFMEERKNQWARKCIGFGNLSVIONKEQAFLT-YHMKDSFTSAWTLNDVNSEH 1018
QY 72 QYMFTD 77
DB 1019 TFLWTD 1024

RESULT 11
LNHUP6
pulmonary surfactant protein A precursor (genomic clone) - human
N/Alternate names: alveolar proteinosis protein; pulmonary surfactant 32K apoprotein; pu
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
C:Accession: A24622; A43628
R:White, R.T.; Damm, D.; Miller, J.; Spratt, K.; Schilling, J.; Hawgood, S.; Benson, B.
Nature 317, 361-363, 1985
A:Title: Isolation and characterization of the human pulmonary surfactant apoprotein gen
A:Reference number: A24622; MUID:86014366; PMID:2995821
A:Accession: A24622
A:Molecule type: DNA
A:Residues: 1-248 <WH1>
A:Cross-references: GB:M0838; NID:G190564; PIDN:AAA36510.1; PID:G190565
A>Note: the sequence in GenBank entry HUMPSAP, release 109.0, (PID:G190565) has the cod
A:Note: four nucleotide differences, producing amino acid differences at positions 45, 5
R:Haegeman, H.P.; White, R.T.; Schilling, J.; Lau, K.; Benson, B.J.; Golden, J.; Hawgood
Am. J. Physiol. 257, L421-L429, 1989
A:Title: Studies of the structure of lung surfactant protein SP-A.
A:Reference number: A43628; MUID:90119861; PMID:2610270
A:Accession: A43628
A:Molecule type: protein
A:Residues: 143-150;220-240;243-248 <HAA>
C:Comment: Pulmonary surfactant is a complex of phospholipids and proteins that lowers t
C:Comment: This protein is a sialoglycoprotein synthesized by alveolar type II cells. It
pendent on the presence of calcium ions.
C:Genetics:
A:Gene: GDB:SFTPA1; SFTPL1; SP-A; SP-A1
A:Cross-references: GDB:119593; OMIM:178630
A:Map position: 10q22-10q23
A:Introns: 58/1; 98/1; 124/1
C:Superfamily: mannose-binding lectin; C-type lectin homology

C:Keywords: alveolar proteinosis; calcium; gaseous exchange; glycoprotein; hydroxylysine
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-248/Product: pulmonary surfactant protein A #status predicted <MAT>
F:28-100/Domain: collagenous #status predicted <COL>
F:127-246/Domain: C-type lectin homology <LCH>
F:206/Disulfide bonds: interchain #status experimental
F:30.33,36.42,57.63,76.79,82,91,97/Modified site: 4-hydroxyproline (Pro) #status predict
F:51.88/Modified site: 5-hydroxylysine (Lys) #status predicted
F:155-246,224-238/Disulfide bonds: #status experimental
F:207/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.8%; Score 78.5; DB 1; Length 248;
Best Local Similarity 28.8%; Pred. No. 0.15;
Matches 15; Conservative 13; Mismatches 23; Indels 1; Gaps 1;

QY 29 CRIRGGLAMPKDEAANTLIADYVAKSGFRVPIGVNDLERGQYMFDTNTP 80
DB 155 CARAGGRIAPRNPENEALASFVKYNTY-AVVGTEGSPGDFRISDGT 205

RESULT 12
LNHUP6
pulmonary surfactant protein A precursor (clone 6A) - human
N/Alternate names: pulmonary surfactant 32K apoprotein; pulmonary surfactant-associated
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
C:Accession: A25720
R:Floros, J.; Steinbrink, R.; Jacobs, K.; Phelps, D.; Kriz, R.; Recny, M.; Sultzman, L.;
J. Biol. Chem. 261, 9029-9033, 1986
A:Title: Isolation and characterization of cDNA clones for the 35-kDa pulmonary surfact
A:Reference number: A25720; MUID:86250832; PMID:3755136
A:Accession: A25720
A:Molecule type: mRNA
A:Residues: 1-248 <FLO>
A:Cross-references: GB:M13686; NID:G190669; PIDN:AAA60211.1; PID:G190670
A>Note: part of the sequence was confirmed by protein sequencing
A>Note: the amino end of the mature protein, which was not identified, is partially acet
A>Note: clones corresponding to two different proteins were sequenced. Cotranslational t
C:Genetics:
A:Gene: GDB:SFTPA1; SFTPL1; SP-A; SP-A1
A:Cross-references: GDB:119593; OMIM:178630
A:Map position: 10q22-10q23
C:Superfamily: mannose-binding lectin; C-type lectin homology
C:Keywords: acetylated amino end; alveolar proteinosis; calcium; gaseous exchange; glyc
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-248/Product: pulmonary surfactant protein A #status predicted <MAT>
F:127-246/Domain: C-type lectin homology <LCH>
F:206/Modified site: acetylated amino end (Glu) (in mature form) #status predicted
F:30.33,36.42,54.57,63.76,79,82,91,97/Modified site: 4-hydroxyproline (Pro) #status pre
F:207/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.8%; Score 78.5; DB 1; Length 248;
Best Local Similarity 28.8%; Pred. No. 0.15;
Matches 15; Conservative 13; Mismatches 23; Indels 1; Gaps 1;

QY 29 CRIRGGLAMPKDEAANTLIADYVAKSGFRVPIGVNDLERGQYMFDTNTP 80
DB 155 CARAGGRIAPRNPENEALASFVKYNTY-AVVGTEGSPGDFRISDGT 205

RESULT 13
LNHUP1
pulmonary surfactant protein A precursor (clone 1A) - human
N/Alternate names: pulmonary surfactant 32K apoprotein; pulmonary surfactant-associated
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
C:Accession: B25720
R:Floros, J.; Steinbrink, R.; Jacobs, K.; Phelps, D.; Kriz, R.; Recny, M.; Sultzman, L.;
J. Biol. Chem. 261, 9029-9033, 1986
A:Title: Isolation and characterization of cDNA clones for the 35-kDa pulmonary surfact
A:Reference number: A25720; MUID:86250832; PMID:3755136
A:Accession: B25720
A:Molecule type: mRNA

A;Residues: 1-248 <FLO>
A;Cross-references: GB:K03475
A;Note: part of the sequence was confirmed by protein sequencing
A;Note: the amino end of the mature protein, which was not identified, is partially acetylated
A;Note: clones corresponding to two different proteins were sequenced. Cotranslational processing
C;Genetics:
A;Gene: GDB:SFTPA1; SFTPL1; SP-A; SP-A1
A;Cross-references: GDB:119593; OMIM:178630
A;Map position: 10q22-10q23
C;Superfamily: mannose-binding lectin; C-type lectin homology
C;Keywords: acetylated amino end; alveolar proteinosis; calcium; gaseous exchange; glycosylation
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-248/Product: pulmonary surfactant protein A #status predicted <MAT>
F;127-246/Domain: C-type lectin homology <LCH>
F;21/Modified site: acetylated amino end (Glu) (in mature form) #status predicted
F;30,33,36,42,54,57,63,76,82,91,97/Modified site: 4-hydroxyproline (Pro) #status predicted
F;207/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.8%; Score 78.5; DB 1; Length 248;
Best Local Similarity 28.8%; Pred. No. 0.15;
Matches 15; Conservative 13; Mismatches 23; Indels 1; Gaps 1;

QY 29 CRIRGMLAMPKDEAANTLIADYVAKSGFFRVFVGNDLREGQYMTDNTP 80
DB 155 CARAGRIAPVPENPEAEIAAFVKYNTY-AYVGLTEGSPGDFRYSDDTP 205

RESULT 14
I51921
pulmonary surfactant-associated protein A1 - human
N;Alternate names: SP-A1
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
C;Accession: I51921
R;Katyal, S.I.; Singh, G.; Locker, J.
A;Title: Characterization of a second human pulmonary surfactant-associated protein SP-A
A;Reference number: I51921; MUID:92198680; PMID:1372511
A;Accession: I51921
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-248 <RES>
A;Cross-references: GB:M68519; NID:g338048; PIDN:AAA60319.1; PID:g338049
C;Genetics:
A;Gene: GDB:SFTPA1; SFTPL1; SP-A; SP-A1
A;Cross-references: GDB:119593; OMIM:178630
A;Map position: 10q22-10q23
A;Introns: 58/1; 98/1; 124/1
C;Superfamily: mannose-binding lectin; C-type lectin homology
F;127-246/Domain: C-type lectin homology <LCH>

Query Match 18.8%; Score 78.5; DB 2; Length 248;
Best Local Similarity 28.8%; Pred. No. 0.15; 23; Indels 1; Gaps 1;
Matches 15; Conservative 13; Mismatches 13; Indels 1; Gaps 1;

QY 29 CRIRGMLAMPKDEAANTLIADYVAKSGFFRVFVGNDLREGQYMTDNTP 80
DB 155 CARAGRIAPVPENPEAEIAAFVKYNTY-AYVGLTEGSPGDFRYSDDTP 205

RESULT 15
JC4031
tetranectin precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Aug-1999
C;Accession: JC4031
R;Sorensen, C.B.; Berglund, L.; Petersen, T.E.
Gene 152, 243-245, 1995
A;Title: Cloning of a cDNA encoding murine tetranectin.
A;Reference number: JC4031; MUID:95137396; PMID:7835708
A;Accession: JC4031
A;Molecule type: mRNA
A;Residues: 1-202 <SOR>

A;Cross-references: EMBL:X79199; NID:g671561; PIDN:CAA55791.1; PID:g671562
A;Experimental source: lung
C;Comment: This protein binds plasminogen, and may play a role in invasive cancer.
C;Superfamily: tetranectin; C-type lectin homology
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-202/Product: tetranectin #status predicted <MAT>
F;71-197/Domain: C-type lectin homology <LCH>

Query Match 18.7%; Score 78; DB 2; Length 202;
Best Local Similarity 27.1%; Pred. No. 0.13; 27; Indels 2; Gaps 1;
Matches 16; Conservative 14; Mismatches 14; Indels 2; Gaps 1;

QY 18 BEKNYRESLTHCRIRGMLAMPKDEAANTLIADYVAKS--GFFRVFVGNDLREGQYM 74
DB 87 QPKTFHEASEDCISQGGTGTGTPQSELEALFVYARHSVGNDAIWLGLNDMAAEGAW 145

Search completed: March 8, 2004, 12:16:21
Job time : 22.1454 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:07:46 ; Search time 20.793 Seconds
(without alignments)
198.629 Million cell updates/sec

Title: US-09-600-932-2_COPY_148_227

Perfect score: 417
Sequence: 1 VIAGRETEKPYIVQSEK.....FIGVNDLEREQYMTDNT 80

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/prodata/2/aaa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/2/aaa/6A_COMB.pep:*
- 4: /cgn2_6/prodata/2/aaa/6B_COMB.pep:*
- 5: /cgn2_6/prodata/2/aaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/prodata/2/aaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98.5	23.6	123	4	US-09-535-521-25
2	98.5	23.6	128	4	US-09-535-521-8
3	98.5	23.6	139	4	US-09-535-521-11
4	98.5	23.6	141	4	US-09-535-521-14
5	98.5	23.6	187	4	US-09-535-521-17
6	98.5	23.6	208	4	US-09-535-521-20
7	98.5	23.6	292	4	US-09-535-521-2
8	98.5	23.6	292	4	US-09-535-521-5
9	88.5	21.2	404	4	US-09-517-605-2
10	85	20.4	197	4	US-09-602-877A-99
11	82	19.7	202	1	US-08-469-486-56
12	82	19.7	202	1	US-08-469-658-56
13	81.5	19.5	1456	4	US-09-976-594-168
14	78	18.7	328	4	US-09-065-040-8
15	78	18.7	328	4	US-09-065-040-12
16	77.5	18.6	118	6	5514582-18
17	76.5	18.3	161	3	US-09-011-735-6
18	76.5	18.3	351	3	US-09-011-735-1
19	76.5	18.3	351	4	US-09-029-156-1
20	74.5	17.9	1479	3	US-08-840-062-2
21	74.5	17.9	1479	3	US-08-840-062-4
22	74	17.7	108	6	5514582-16
23	73	17.5	1722	4	US-09-194-612A-1
24	72.5	17.4	337	4	US-09-489-039A-13994
25	72	17.3	323	4	US-09-065-040-4
26	71.5	17.1	145	3	US-08-772-440-14
27	71.5	17.1	1487	3	US-08-840-062-7

28 71 17.0 107 6 5514582-17
29 70.5 16.9 125 3 US-08-722-126A-7
30 70.5 16.9 125 5 PCT-US95-04258-7
31 70.5 16.9 287 1 US-08-365-103B-4
32 70.5 16.9 300 1 US-08-365-103B-6
33 70.5 16.9 327 1 US-08-365-103B-2
34 69.5 16.7 110 6 5514582-9
35 69.5 16.7 114 3 US-08-722-126A-6
36 69.5 16.7 114 5 PCT-US95-04258-6
37 69.5 16.7 188 3 US-08-722-126A-5
38 69.5 16.7 188 5 PCT-US95-04258-5
39 69.5 16.7 1463 1 US-08-220-603A-11
40 68 16.3 1209 5 PCT-US95-04589-107
41 68 16.3 1258 2 US-08-310-912A-107
42 68 16.3 1258 3 US-09-301-085-107
43 68 16.3 1294 3 US-08-930-996A-10
44 67 16.1 131 3 US-08-772-440-23
45 67 16.1 131 3 US-08-772-440-27

ALIGNMENTS

RESULT 1
US-09-535-521-25
; Sequence 25, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-535-521-25

Query Match 23.6%; Score 98.5; DB 4; Length 123;
Best Local Similarity 30.6%; Pred. No. 8.9e-06;
Matches 22; Conservative 14; Mismatches 33; Indels 3; Gaps 1;
QY 9 EKFTYIVQSEKPYIVQSEKTHORIRGGMLAMPKDAANTLIADYVAKSGPFRVFIGVNDLE 68
DB 14 QRKCYFGEPEPKMIOAFACSKLQGRLASIHSEQEDFLARYANKKG---TWIGRLDLD 70
QY 69 REGQYMTDNT 80
DB 71 REGEFINDENP 82

RESULT 2
US-09-535-521-8
; Sequence 8, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26

	Matches	22; Conservative	14; Mismatches	33; Indels	3; Gaps	1;
QY	9	E E E Y I V Q E K N Y R S L T H C R I R G N L A M P X D E A A N T L I A D Y A K S G F F V F I G W N D L E	:	:	:	68
Db	175	Q R C Y Y P G E E P F K W I O A R F A C S K L Q R L A S I H S Q E Q D F L A R Y A N K G - - - T W I G L R D L D	:	:	:	231
QY	69	R E Q Y M F T D N T P	:	:	:	80
Db	232	R E G E F I W N D E N P	:	:	:	243

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RESULT 9
US-09-517-605-2
; Sequence 2, Application US/09517605
; Patent No. 6391567
; GENERAL INFORMATION:
; APPLICANT: Littman, Dan R.
; APPLICANT: Kwon, Douglas S.
; APPLICANT: van Kooyk
; APPLICANT: Geijtenbeck, Theo
; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 1049-1-017
; CURRENT APPLICATION NUMBER: US/09/517,605
; CURRENT FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-517-605-2

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	Query Match	21-2%;	Score 88.5;	DB 4;	Length 404;
	Best Local Similarity	25.0%;	Pred No. 0,0011;		
	Matches	17;	Conservative	20;	Mismatches 30; Indels 1; Gaps 1;
OY	13	YYVQEKNTRESLTCRTRGGNLAMPDEAANTLIADYVAKSGFFRVFTGVNDLEREQ	72		
DB	268	YFMSNGRNWHDISITAKEVGAGLVIVIKSBEONFLQLQSRSNRF-TWMGLSDLNQEGT	326		
OY	73	YMETDNTPT	80		
DB	327	WOWVDGSP	334		

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RESULT 10
US-03-602-877A-99
; Sequence 99, Application US/09502877A
; Patent No. 6432707
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.446C5
; CURRENT APPLICATION NUMBER: US/09/602,877A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 99
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-602-877A-99

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Query Match      20.4%; Score 85; DB 4; Length 197;  
Best Local Similarity 25.7%; Pred. No. 0.0012;  
Matches 18; Conservative 20; Mismatches 30; Indels 2; Gaps 1;  
  
QY          7 ETEKFYYVQEKNRYRESLTHCRIRGGNLMAMPKDEAANTLIADYAKS--GFPRVFPIGV 64  
          : * : : : : : : : : : : : : : : : : :  
          : : : : : : : : : : : : : : : : : :
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; LENGTH: 1456
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1674368CD1
US-09-976-594-168

Query Match
Best Local Similarity 19.5%; Score 81.5; DB 4; Length 1456;
Matches 19; Conservative 15; Mismatches 31; Indels 1; Gaps 1;

QY 12 FYIVQEKNYRESLTHCRIRGGMLAMPKDEAAANTLIADYVAKSGFRVFGVNDLREG 71
Db 960 FGFMEERKNQWEAKACIGFNGNLVSIQNEKEQAFIT-YHKDSTFSAWTGLNDVNSEH 1018
QY 72 QYMTD 77
Db 1019 TELMTD 1024

RESULT 14
US-09-065-040-8
; Sequence 8, Application US/09065040
; Patent No. 6541217
; GENERAL INFORMATION:
; APPLICANT: Hiraoka, Atsunobu
; APPLICANT: Sugimura, Atsushi
; APPLICANT: Mio, Hiroyuki
; TITLE OF INVENTION: HEMATOPOIETIC STEM CELL GROWTH FACTOR
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
; ADDRESSEE: DUNNER, LLP
; STREET: 1300 I Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/065,040
; FILING DATE: 27-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 087242/1997
; FILING DATE: 27-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 262252/1996
; FILING DATE: 27-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Fordis, Jean B.
; REGISTRATION NUMBER: 32,984
; REFERENCE/DOCKET NUMBER: 04853.0026-00000
; TELEPHONE: 202-408-4400
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-065-040-8

Query Match
Best Local Similarity 18.7%; Score 78; DB 4; Length 328;
Matches 21; Conservative 19; Mismatches 33; Indels 4; Gaps 3;

QY 2 IAGIRETEEKFYIVQBEKNYRESLTHCRIRGGMLAMPKDEAAANTLIADYV--AKSGF-F 58
Db 183 LKGLR-LGKCFILSRDFETQAAAQARCKARGGSLAQPADRQMDALSRYLRAALAPYNW 241
QY 59 RVFIGVNDLREGQYMF 75
Db 242 PVLGVHDDRSEGLYLF 258

Query Match
Best Local Similarity 18.7%; Score 78; DB 4; Length 328;
Matches 21; Conservative 19; Mismatches 33; Indels 4; Gaps 3;

QY 2 IAGIRETEEKFYIVQBEKNYRESLTHCRIRGGMLAMPKDEAAANTLIADYV--AKSGF-F 58
Db 183 LKGLR-LGKCFILSRDFETQAAAQARCKARGGSLAQPADRQMDALSRYLRAALAPYNW 241
QY 59 RVFIGVNDLREGQYMF 75
Db 242 PVLGVHDDRSEGLYLF 258

RESULT 15
US-09-065-040-12
; Sequence 12, Application US/09065040
; Patent No. 6541217
; GENERAL INFORMATION:
; APPLICANT: Hiraoka, Atsunobu
; APPLICANT: Sugimura, Atsushi
; APPLICANT: Mio, Hiroyuki
; TITLE OF INVENTION: HEMATOPOIETIC STEM CELL GROWTH FACTOR
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
; ADDRESSEE: DUNNER, LLP
; STREET: 1300 I Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/065,040
; FILING DATE: 27-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 262252/1996
; FILING DATE: 27-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 087242/1997
; FILING DATE: 24-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP97/02349
; FILING DATE: 07-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Fordis, Jean B.
; REGISTRATION NUMBER: 32,984
; REFERENCE/DOCKET NUMBER: 04853.0026-00000
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-065-040-12

Query Match
Best Local Similarity 27.3%; Score 78; DB 4; Length 328;
Matches 21; Conservative 19; Mismatches 33; Indels 4; Gaps 3;

QY 2 IAGIRETEEKFYIVQBEKNYRESLTHCRIRGGMLAMPKDEAAANTLIADYV--AKSGF-F 58
Db 183 LKGLR-LGKCFILSRDFETQAAAQARCKARGGSLAQPADRQMDALSRYLRAALAPYNW 241
QY 59 RVFIGVNDLREGQYMF 75
Db 242 PVLGVHDDRSEGLYLF 258
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Db 242 PVWLGVHRRSEGLYLF 258

Search completed: March 8, 2004, 12:17:28
Job time : 20.793 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: March 8, 2004, 11:54:00 ; Search time 73.6564 Seconds
(without alignments)
306.882 Million cell updates/sec

Title: US-09-600-932-2_COPY_148_227
Perfect score: 417
Sequence: 1 VIAGIRETEREFYIVQEK.....FIGVNDLEREGQYMTDNT 80

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Genesep1980s.*
2: Genesep1990s.*
3: Genesep2000s.*
4: Genesep2001s.*
5: Genesep2002s.*
6: Genesep2003as.*
7: Genesep2003bs.*
8: Genesep2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	417	100.0	277	2	AAV25518	Aay25518 Human col
3	409	98.1	277	2	AAV41698	Aay41698 Human PRO
4	409	98.1	277	3	AB44254	Aab44254 Human PRO
5	409	98.1	277	4	AAU29073	Aau29073 Human PRO
6	409	98.1	277	6	ABU58449	Abu58449 Human PRO
7	409	98.1	277	6	ABU87997	Abu87997 Novel hum
8	409	98.1	277	6	ABU84312	Abu84312 Human sec
9	409	98.1	277	6	ABR66186	Abu66186 Human sec
10	409	98.1	277	6	ABR65576	Abu65576 Human sec
11	409	98.1	277	6	ABU93516	Abu93516 Human sec
12	409	98.1	277	6	ABU82755	Abu82755 Human PRO
13	409	98.1	277	6	ABU89876	Abu89876 Novel hum
14	409	98.1	277	6	ABR68125	Abu68125 Human sec
15	409	98.1	277	6	ABU96178	Abu96178 Novel hum
16	409	98.1	277	6	ABU92609	Abu92609 Human sec
17	409	98.1	277	6	ABO08686	Abu08686 Human sec
18	409	98.1	277	6	ABO02738	Abu02738 Human sec
19	409	98.1	277	6	ABR74892	Abu74892 Human sec
20	409	98.1	277	6	ABR94654	Abu94654 Human sec
21	409	98.1	277	6	ABO25200	Abu25200 Novel hum
22	409	98.1	277	6	ABU85627	Abu85627 Novel hum
23	409	98.1	277	6	ABU98787	Abu98787 Novel hum
24	409	98.1	277	6	ABU98002	Abu98002 Novel hum
25	409	98.1	277	6	ABU91708	Abu91708 Novel hum

26	409	98.1	277	6	ABU72206	Novel hum
27	409	98.1	277	6	ABU89401	Abu89401 Human PRO
28	409	98.1	277	6	ABU86242	Abu86242 Human sec
29	409	98.1	277	6	ABU67455	Abu67455 Human sec
30	409	98.1	277	6	ABU80483	Abu80483 Human PRO
31	409	98.1	277	6	ABR99401	Abu99401 Human sec
32	409	98.1	277	6	ABR98791	Abu98791 Human sec
33	409	98.1	277	6	ABO16314	Abu16314 Human sec
34	409	98.1	277	6	ABR92214	Abu92214 Human sec
35	409	98.1	277	6	ABO18855	Abu18855 Human sec
36	409	98.1	277	6	ABR78276	Abu78276 Human sec
37	409	98.1	277	6	ABU85012	Abu85012 Novel hum
38	409	98.1	277	6	ABO00151	Abu000151 Novel hum
39	409	98.1	277	6	ABO11483	Abu11483 Human sec
40	409	98.1	277	6	ABO2123	Abu02123 Human sec
41	409	98.1	277	6	ABU86702	Abu86702 Novel hum
42	409	98.1	277	6	ABU83397	Abu83397 Human sec
43	409	98.1	277	6	ABO06198	Abu06198 Novel hum
44	409	98.1	277	6	ABR59234	Abu59234 Human sec
45	409	98.1	277	6	ABO09296	Abu09296 Human sec

ALIGNMENTS

RESULT 1
ABB56404
ID ABB56404 standard; peptide; 159 AA.
XX ABB56404;
AC ABB56404;
XX
DT 19-FEB-2002 (first entry)
XX
DE Human collectin polypeptide SEQ ID NO 52.
XX
KW Human; collectin; CL-L2-1; CL-L2-2; mouse; antibacterial; virucide;
KW protein therapy; infection; ds.
XX
OS Homo sapiens.
XX
PN WO200181401-A1.
XX
PD 01-NOV-2001.
XX
PF 23-APR-2001; 2001WO-JP003468.
XX
PR 21-APR-2000; 2000JP-00120358.
XX
(FUSO) FUSO PHARM IND LTD.
XX
Wakamiya N, Keshi H, Ontani K, Sakamoto T, Kishi Y;
DR WPI; 2002-055345/07.
XX
New collectin family proteins, designated CL-L2-1 and CL-L2-2, expressed
in kidney and for treatment and prevention of bacterial and viral
infections.
XX
Claim 8; Page 68; 134pp; Japanese.
XX
The invention relates to human collectin family proteins (CL-L2-1 and CL-
L2-2, sequences given in the specification, ABB56407-ABB56411 and
CC ABB56414-ABB56416), their derivatives and fragments and a related
CC collectin (CL-L2) of mouse origin (ABB56412) and polynucleotides encoding
CC all or part of the proteins. The proteins have antibacterial and virucide
CC activity and are used for protein therapy and treatment, prevention and
CC diagnosis of bacterial and viral infections. The present sequence is that
CC of a collectin polynucleotide of the invention
SQ Sequence 159 AA;
Query Match 100.0%; Score 417; DB 5; Length 159;
Best Local Similarity 100.0%; Pred. No. 4.5e-47;

Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIAGIRETEKEFYIYQBEKNYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFFRV 60
 |||||
 Db 30 VIAGIRETEKEFYIYQBEKNYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFFRV 89
 |||||

QY 61 FIGVNDLEREGQWFTDNTP 80
 |||||
 Db 90 FIGVNDLEREGQWFTDNTP 109
 |||||

RESULT 2
 AAY25518
 ID AAY25518 standard; protein; 277 AA.
 XX
 AC AAY25518;
 XX
 DT 30-SEP-1999 (first entry)
 XX
 DE Human collectin protein.
 XX
 KW Collectin; human; antibacterial; antiviral; treatment; infection.
 XX
 OS Homo sapiens.
 XX
 PN WO9937767-A1.
 PD 29-JUL-1999.
 XX
 PF 24-JUL-1998; 98WO-JP003328.
 XX
 PR 23-JAN-1998; 98JP-00011281.
 XX
 PA (FUSO) FUSO PHARM IND LTD.
 XX
 PI Wakamiya N;
 XX
 DR WPI; 1999-458691/38.
 DR N-PSDB; AAX88323.
 XX
 PT New collectin protein of human origin and DNA encoding it.
 XX
 PS Claim 1; Page 42-44; 58pp; Japanese.
 XX
 CC This invention describes the isolation and characterisation of a novel
 CC human collectin protein and its encoding polynucleotide. The human
 CC collectin exhibits antibacterial and antiviral activity and can be used
 CC as an agent for the treatment of human bacterial and viral infections.
 CC This sequence represents the novel human collectin
 XX
 SQ Sequence 277 AA;

Query Match 100.0%; Score 417; DB 2; Length 277;
 Best Local Similarity 100.0%; Pred. No. 9.8e-47;
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIAGIRETEKEFYIYQBEKNYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFFRV 60
 |||||
 Db 148 VIAGIRETEKEFYIYQBEKNYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFFRV 207
 |||||

QY 61 FIGVNDLEREGQWFTDNTP 80
 |||||
 Db 208 FIGVNDLEREGQWFTDNTP 227
 |||||

RESULT 3
 AAY41698
 ID AAY41698 standard; protein; 277 AA.
 XX
 AC AAY41698;
 XX
 DT 07-DEC-1999 (first entry)
 XX

DE Human PRO702 protein sequence.
 XX
 KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
 KW secreted protein; transmembrane protein.
 XX
 OS Homo sapiens.
 XX
 PN WO9946281-A2.
 PD 16-SEP-1999.
 XX
 PF 08-MAR-1999; 99WO-US005028.
 XX
 PR 10-MAR-1998; 98US-0077450P.
 PR 11-MAR-1998; 98US-0077632P.
 PR 11-MAR-1998; 98US-0077641P.
 PR 11-MAR-1998; 98US-0077649P.
 PR 12-MAR-1998; 98US-0077791P.
 PR 13-MAR-1998; 98US-0078004P.
 PR 17-MAR-1998; 98US-00040220.
 PR 20-MAR-1998; 98US-0078886P.
 PR 20-MAR-1998; 98US-0078910P.
 PR 20-MAR-1998; 98US-0078936P.
 PR 20-MAR-1998; 98US-0078939P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 26-MAR-1998; 98US-0079656P.
 PR 27-MAR-1998; 98US-0079663P.
 PR 27-MAR-1998; 98US-0079664P.
 PR 27-MAR-1998; 98US-0079689P.
 PR 27-MAR-1998; 98US-0079728P.
 PR 27-MAR-1998; 98US-0079786P.
 PR 30-MAR-1998; 98US-0079920P.
 PR 30-MAR-1998; 98US-0079923P.
 PR 31-MAR-1998; 98US-0080105P.
 PR 31-MAR-1998; 98US-0080107P.
 PR 31-MAR-1998; 98US-0080165P.
 PR 31-MAR-1998; 98US-0080194P.
 PR 01-APR-1998; 98US-0080327P.
 PR 01-APR-1998; 98US-0080328P.
 PR 01-APR-1998; 98US-0080333P.
 PR 01-APR-1998; 98US-0080334P.
 PR 08-APR-1998; 98US-0081049P.
 PR 08-APR-1998; 98US-0081070P.
 PR 08-APR-1998; 98US-0081071P.
 PR 09-APR-1998; 98US-0081135P.
 PR 09-APR-1998; 98US-0081203P.
 PR 09-APR-1998; 98US-0081229P.
 PR 15-APR-1998; 98US-0081817P.
 PR 15-APR-1998; 98US-0081838P.
 PR 15-APR-1998; 98US-0081952P.
 PR 15-APR-1998; 98US-0081955P.
 PR 21-APR-1998; 98US-0082568P.
 PR 21-APR-1998; 98US-0082569P.
 PR 22-APR-1998; 98US-0082700P.
 PR 22-APR-1998; 98US-0082704P.
 PR 22-APR-1998; 98US-0082804P.
 PR 23-APR-1998; 98US-0082767P.
 PR 23-APR-1998; 98US-0082796P.
 PR 27-APR-1998; 98US-0083336P.
 PR 28-APR-1998; 98US-0083332P.
 PR 29-APR-1998; 98US-0083392P.
 PR 29-APR-1998; 98US-0083495P.
 PR 29-APR-1998; 98US-0083496P.
 PR 29-APR-1998; 98US-0083499P.
 PR 29-APR-1998; 98US-0083500P.
 PR 29-APR-1998; 98US-0083545P.
 PR 29-APR-1998; 98US-0083554P.
 PR 29-APR-1998; 98US-0083558P.
 PR 29-APR-1998; 98US-0083559P.
 PR 30-APR-1998; 98US-0083742P.
 PR 05-MAY-1998; 98US-0084366P.
 PR 06-MAY-1998; 98US-0084414P.

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PR 06-MAY-1998;          98US-0084441P.
PR 07-MAY-1998;          98US-0084598P.
PR 07-MAY-1998;          98US-0084600P.
PR 07-MAY-1998;          98US-0084627P.
PR 07-MAY-1998;          98US-0084637P.
PR 07-MAY-1998;          98US-0084639P.
PR 07-MAY-1998;          98US-0084640P.
PR 07-MAY-1998;          98US-0084643P.
PR 13-MAY-1998;          98US-0085323P.
PR 13-MAY-1998;          98US-0085338P.
PR 13-MAY-1998;          98US-0085339P.
PR 15-MAY-1998;          98US-0085573P.
PR 15-MAY-1998;          98US-0085579P.
PR 15-MAY-1998;          98US-0085580P.
PR 15-MAY-1998;          98US-0085582P.
PR 15-MAY-1998;          98US-0085683P.
PR 15-MAY-1998;          98US-0085697P.
PR 15-MAY-1998;          98US-0085700P.
PR 15-MAY-1998;          98US-0085704P.
PR 18-MAY-1998;          98US-0086023P.
PR 22-MAY-1998;          98US-0086032P.
PR 22-MAY-1998;          98US-0086414P.
PR 22-MAY-1998;          98US-0086430P.
PR 22-MAY-1998;          98US-0086485P.
PR 26-MAY-1998;          98US-0087098P.
PR 28-MAY-1998;          98US-0087106P.
PR 28-MAY-1998;          98US-0087208P.
PR 30-JUL-1998;          98US-0094651P.
PR 11-SEP-1998;          98US-0100038P.
XX
XX
XX (GETH ) GENENTECH INC.
XX
XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
PI WPI; 1999-551358/46.
XX N-PSDB; AAZ33973.
DR
XX
XX New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders.
XX
XX Claim 12; Fig 37; 530pp; English.
XX
XX The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as sources
CC of probes, primers, for chromosome mapping, and for generation of
CC antisense sequences. They can also be used to create transgenic animals.
CC The proteins can be used to treat a variety of diseases and disorders.
CC depending on their function. Diseases that may be treated include blood
CC coagulation disorders, cancers and cellular adhesion disorders. They may
CC also be used to raise antibodies. AAZ33891 to AAZ3438, and AAZ41685 to
CC AAZ41774 represent polynucleotide and polypeptide sequence given in the
XX exemplification of the present invention
XX
XX Sequence 277 AA;
SQ
Query Match          98.1%; Score 409; DB 2; Length 277;
Best Local Similarity 98.8%; Pred. No. 1.1e-45;
Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 VIAGIRETEEFYYIVQEKNYRESLTHCRIRGMLAMPKDEAANTLIADYYVAKSGFFRV 60
DB 148 VIAGIRETEEFYYIVQEKNYRESLTHCRIRGMLAMPKDEAANTLIADYYVAKSGFFRV 207
OY 61 FIGVNDLRREGQYMTDNTNP 80
DB 208 FIGVNDLRREGQYMTDNTNP 227
XX
RESULT 4
AAB44254
ID AAB44254 standard; protein; 277 AA.
XX

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Db 148 VIAGIRETEKFFYIVQEEKNYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFFRV 207
QY 61 FIGVNDLEREGQYMTDNT 80
|||||
Db 208 FIGVNDLEREGQYMTDNT 227
|||||
RESULT 5
AAU29073
ID AAU29073 standard; protein; 277 AA.
XX AAU29073;
AC AAU29073;
XX
DT 19-DEC-2001 (first entry)
XX
DE Human PRO polypeptide sequence #50.
XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200168848-A2.
XX
PD 20-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006520.
XX
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 06-MAR-2000; 2000US-0186968P.
PR 14-MAR-2000; 2000US-0189320P.
PR 14-MAR-2000; 2000US-0189328P.
PR 15-MAR-2000; 2000WO-US006884.
PR 21-MAR-2000; 2000US-0190828P.
PR 21-MAR-2000; 2000US-0191007P.
PR 21-MAR-2000; 2000US-0191048P.
PR 21-MAR-2000; 2000US-0191314P.
PR 28-MAR-2000; 2000US-0192655P.
PR 29-MAR-2000; 2000US-0193032P.
PR 29-MAR-2000; 2000US-0193053P.
PR 30-MAR-2000; 2000WO-US0008439.
PR 04-APR-2000; 2000US-0194449P.
PR 04-APR-2000; 2000US-0194647P.
PR 11-APR-2000; 2000US-0195975P.
PR 11-APR-2000; 2000US-0196000P.
PR 11-APR-2000; 2000US-0196187P.
PR 11-APR-2000; 2000US-0196890P.
PR 11-APR-2000; 2000US-0196820P.
PR 18-APR-2000; 2000US-0198121P.
PR 18-APR-2000; 2000US-0198585P.
PR 25-APR-2000; 2000US-0199397P.
PR 25-APR-2000; 2000US-0199550P.
PR 25-APR-2000; 2000US-0199654P.
PR 03-MAY-2000; 2000US-0201516P.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
XX
XX (GETH) GENENTECH INC.
PA Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI

PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2001-602746/68.
DR N-PSDB; AAS45974.
XX
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.
XX
XX Claim 11; Fig 100; 774pp; English.
XX
XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumour in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders
XX
XX Sequence 277 AA;
SQ
Query Match 98.1%; Score 409; DB 4; Length 277;
Best Local Similarity 98.8%; Pred. No. 1.1e-45;
Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VIAGIRETEKFFYIVQEEKNYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFFRV 60
|||||
Db 148 VIAGIRETEKFFYIVQEEKNYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFFRV 207
|||||
QY 61 FIGVNDLEREGQYMTDNT 80
|||||
Db 208 FIGVNDLEREGQYMTDNT 227
|||||
RESULT 6
ABUS8449
ID ABUS8449 standard; protein; 277 AA.
XX
XX ABUS8449;
XX
XX 15-APR-2003 (first entry)
DT
XX
XX Human PRO polypeptide #50.
DE
XX
KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX
XX Homo sapiens.
OS
XX
XX US2003027272-A1.
PN
XX
XX 06-FEB-2003.
PD
XX
XX 21-JUN-2002; 2002US-00176492.
PF
XX
XX 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059286P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.

PR	28-OCT-1997;	97US-0063544P.	PR	11-JUN-1998;	98US-0088876P.
PR	28-OCT-1997;	97US-0063564P.	PR	12-JUN-1998;	98US-0089090P.
PR	29-OCT-1997;	97US-0063734P.	PR	12-JUN-1998;	98US-0089105P.
PR	31-OCT-1997;	97US-0063870P.	PR	16-JUN-1998;	98US-0089512P.
PR	31-OCT-1997;	97US-0064103P.	PR	16-JUN-1998;	98US-0089514P.
PR	13-NOV-1997;	97US-0065311P.	PR	17-JUN-1998;	98US-0089538P.
PR	21-NOV-1997;	97US-0066120P.	PR	17-JUN-1998;	98US-0089598P.
PR	24-NOV-1997;	97US-0066466P.	PR	17-JUN-1998;	98US-0089653P.
PR	24-NOV-1997;	97US-0066772P.	PR	18-JUN-1998;	98US-0089908P.
PR	11-DEC-1997;	97US-0069333P.	PR	19-JUN-1998;	98US-0089952P.
PR	12-DEC-1997;	97US-0069425P.	PR	22-JUN-1998;	98US-0090246P.
PR	17-DEC-1997;	97US-0069870P.	PR	22-JUN-1998;	98US-0090252P.
PR	18-DEC-1997;	97US-0068017P.	PR	22-JUN-1998;	98US-0090254P.
PR	10-MAR-1998;	98US-0077450P.	PR	24-JUN-1998;	98US-0090429P.
PR	11-MAR-1998;	98US-0077532P.	PR	24-JUN-1998;	98US-0090435P.
PR	11-MAR-1998;	98US-0077649P.	PR	24-JUN-1998;	98US-0090444P.
PR	20-MAR-1998;	98US-0078888P.	PR	24-JUN-1998;	98US-0090461P.
PR	20-MAR-1998;	98US-0078939P.	PR	24-JUN-1998;	98US-0090535P.
PR	27-MAR-1998;	98US-0079664P.	PR	24-JUN-1998;	98US-0090540P.
PR	27-MAR-1998;	98US-0079786P.	PR	25-JUN-1998;	98US-0090676P.
PR	31-MAR-1998;	98US-0080107P.	PR	25-JUN-1998;	98US-0090678P.
PR	31-MAR-1998;	98US-0080194P.	PR	25-JUN-1998;	98US-0090688P.
PR	01-APR-1998;	98US-0080327P.	PR	25-JUN-1998;	98US-0090690P.
PR	01-APR-1998;	98US-0080333P.	PR	25-JUN-1998;	98US-0090694P.
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PR	08-APR-1998;	98US-0081070P.	PR	25-JUN-1998;	98US-0090696P.
PR	09-APR-1998;	98US-0081195P.	PR	26-JUN-1998;	98US-0090862P.
PR	15-APR-1998;	98US-0081838P.	PR	26-JUN-1998;	98US-0090863P.
PR	21-APR-1998;	98US-0082568P.	PR	26-JUN-1998;	98US-0091010P.
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PR	22-APR-1998;	98US-0082797P.	PR	02-JUL-1998;	98US-0091478P.
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PR	29-APR-1998;	98US-0083499P.	PR	02-JUL-1998;	98US-0091632P.
PR	05-MAY-1998;	98US-0083559P.	PR	04-AUG-1998;	98US-0095282P.
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PR	06-MAY-1998;	98US-0084414P.	PR	10-AUG-1998;	98US-0096012P.
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PR	28-MAY-1998;	98US-0087208P.	PR	26-AUG-1998;	98US-0097971P.
PR	02-JUN-1998;	98US-0087609P.	PR	26-AUG-1998;	98US-0097974P.
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QY 61 FIGVNDLREGQVMTDNTP 80
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XX KW Human; secreted and transmembrane protein: PRO; gene therapy;
XX KW tumour necrosis factor-alpha release; TNF-alpha release;
XX KW chondrocyte proliferation; chondrocyte differentiation; tumour;
XX KW adrenal tumour; lung tumour; colon tumour; breast tumour;
XX KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX OS Homo sapiens.
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XX PD 13-FEB-2003.
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Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 FIGVNDLEREGQYMTDNTP 80
Db 208 FIGVNDLEREGQYMTDNTP 227

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AC ABU84312;
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DT 02-AUG-2003 (first entry)
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DE Human secreted/transmembrane protein (PRO) #50.
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KW Human; secreted and transmembrane protein; PRO; TNF-alpha;
XX tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
XX tissue typing.
OS Homo sapiens.
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PD 13-FEB-2003.
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KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
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KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnery; gene therapy.
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XX extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnery; gene therapy.
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Db 208 FIGVNDLEREGYMTDNTP 227

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KW Human; PRO polypeptide; secreted and transmembrane protein; tumour;
chromosome mapping; gene mapping; cytostatic.
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OS Homo sapiens.
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PN US2003032113-A1.
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PD 13-FEB-2003.
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Best Local Similarity 98.8%; Pred. No. 1.le-45;
Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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XX AC ABUS9876;
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XX DT 11-AUG-2003 (first entry)
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XX KM chondrocyte differentiation; tumour necrosis factor-alpha release;
XX KW affinity purification.
XX
XX OS Homo sapiens.
XX
XX PN US2003036147-A1.
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XX PF 02-JUL-2002; 2002US-00187741.
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Db 208 FIGVNDLREGQYMTDNTTP 227

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AC ABR68125;
XX
DT 11-AUG-2003 (first entry)
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XX
KW Human; PRO; secreted protein; transmembrane protein;
extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
chondrocyte; proliferation; differentiation; cartilage disorder;
bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
adrenal tumour; lung; colon; breast; kidney; rectum; cervix;
liver; drug screening; transgenic animal; genetic analysis;
antiarthritic; vulnary; gene therapy.
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XX
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XX KW knockout; chromosome identification; tissue typing; tumour;
XX KW chondrocyte proliferation; chondrocyte differentiation;
XX KW tumor necrosis factor-alpha release stimulator.
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Job time : 73.6564 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:11:31 ; Search time 28.987 Seconds

(without alignments)
584,534 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 809742

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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; Publication No. US20030158382A1
; GENERAL INFORMATION:
; APPLICANT: Wakamiya et al.
; TITLE OF INVENTION: NO. US20030158382A1e1 Collectin
; FILE REFERENCE: 19036/38785
; CURRENT APPLICATION NUMBER: US/10/258,105
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: PCT/JP01/03468
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: JP 2000-120358
; NUMBER OF SEQ ID NOS: 61
; SEQ ID NO 14
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Known CRD amino acid sequence of reported CL-L1 which was employed for searching EST data base.
US-10-258-105-14

Query Match 100.0%; Score 417; DB 14; Length 159;
Best Local Similarity 100.0%; Pred. NO. 2e-45; Indels 0; Gaps 0;
Matches 80; Conservative 0; Mismatches 0;
QY 1 VIAGIRETEKFFYIVQEKKNYRESLTHCRIGRGLAMPKDEAANTLIADYVAKSGFFRV 60
Db 30 VIAGIRETEKFFYIVQEKKNYRESLTHCRIGRGLAMPKDEAANTLIADYVAKSGFFRV 89
QY 61 FIGVNDLEREGQYMTDNT 80
Db 90 FIGVNDLEREGQYMTDNT 109

RESULT 2

US-09-978-295A-97
; Sequence 97, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kjavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
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52	PRIOR FILING DATE: 1998-05-15	
53	PRIOR APPLICATION NUMBER: 60/085704	
54	PRIOR FILING DATE: 1998-05-15	
55	PRIOR APPLICATION NUMBER: 60/085697	

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.

TITLE OF INVENTION: Acids and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same

FILE REFERENCE: P2630PIC27

CURRENT APPLICATION NUMBER: US/09/978,697

CURRENT FILING DATE: 2001-10-16

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

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; PRIOR FILING DATE: 1998-05-15
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Query Match 98.1%; Score 409; DB 9; Length 277;

Best Local Similarity 98.8%; Pred. No. 4.3e-44; Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VIAGIRETEEFYIVQEKYRESLTHCRIRGKMLAMPKDEAANTLIADYVAKSGPFRV 60
Db 148 VIAGIRETEEFYIVQEKYRESLTHCRIRGKMLAMPKDEAANTLIADYVAKSGPFRV 207

Qy 61 FIGVNDLREGGQYMETDNTTP 80
Db 208 FIGVNDLREGGQYMETDNTTP 227

RESULT 4

US-09-978-192A-97
; Sequence 97, Application US/09978192A
; Patent No. US2002017753A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrata, Napoleon
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APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
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PRIOR FILING DATE: 1998-04-29
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 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.1%; Score 409; DB 9; Length 277;
 Best Local Similarity 98.8%; Pred. No. 4.3e-44;
 Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VIAGIRTESEKYYIYOENKKNYESTHCRIRGGLAMPKDEAANTLIADYVAKSGPFRV 60
 Db 148 VIAGIRTESEKYYIYOENKKNYESTHCRIRGGLAMPKDEAANTLIADYVAKSGPFRV 207
 Qy 61 FIGVNDLEREGQYMTDNTTP 80
 Db 208 FIGVNDLEREGQYMTDNTTP 227

RESULT 5
 US-09-999-832A-97
 ; Sequence 97, Application US/09999832A
 ; Publication No. US20020192706A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630PIC63
 CURRENT APPLICATION NUMBER: US/09/999,832A
 CURRENT FILING DATE: 2001-10-24
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.1%; Score 409; DB 9; Length 277;

Best Local Similarity 98.8%; Pred. No. 4.3e-44; Mismatches 0; Indels 0; Gaps 0;

Matches 79; Conservative 0;

QY 1 VIAGIRETEKFFYIVQEKKNYRESLTHCRIGMMLAMPKDEAANTLIADYVAKSGFFRV 60

Db 148 VIAGIRETEKFFYIVQEKKNYRESLTHCRIGMMLAMPKDEAANTLIADYVAKSGFFRV 207

QY 61 FIGVNDLEREGQYMTDNTP 80

Db 208 FIGVNDLEREGQYMTDNTP 227

RESULT 6

US-09-978-189-97
; Sequence 97, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630F1C7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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PRIOR FILING DATE: 1998-04-29
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PRIOR FILING DATE: 1998-04-29

1. GERTTSEN, Mary E. ?
2. APPLICANT: GERTTSEN, Mary E. ?
3. APPLICANT: Garber, Hanspeter ?
4. APPLICANT: Gao, Wei-Qiang ?
5. APPLICANT: Fong, Sherman ?
6. APPLICANT: Filvaroff, Ellen ?
7. APPLICANT: Ferrari, Napoleon ?
8. APPLICANT: Eaton, Dan ?
9. APPLICANT: Desnoyers, Luc ?
10. APPLICANT: Botschein, David ?
11. APPLICANT: Baker Kevin P. ?
12. APPLICANT: Ashkenazi, Avi ?

/ APPLICANT: Ashkenazi, Avi
 / APPLICANT: Baker Kevin P.
 / APPLICANT: Botstein, David
 / APPLICANT: Desnoyers, Luc
 / APPLICANT: Eaton, Dan
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 / APPLICANT: Goddard, Audrey
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 / APPLICANT: Grimaldi, J. Christopher
 / APPLICANT: Gurney, Austin L.
 / APPLICANT: Hillan, Kenneth J.
 / APPLICANT: Kiljavin, Ivar J.
 / APPLICANT: Kuo, Sophia S.
 / APPLICANT: Napier, Mary A.
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 / APPLICANT: Paoni, Nicholas F.
 / APPLICANT: Roy, Margaret Ann
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 / APPLICANT: Stewart, Timothy A.
 / APPLICANT: Tumas, Daniel
 / APPLICANT: Williams, P. Mickey

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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC15
CURRENT APPLICATION NUMBER: US/09/978,585A
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrapper or Palm
SEQ ID NO 97
LENGTH: 277
TYPE: PRT
ORGANISM: Homo sapiens
US-09-978-585A-97

Query Match 98.1%; Score 409; DB 10; Length 277;
Best Local Similarity 98.8%; Pred. No. 4.3e-44;
Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VIAGIRETEKFIYVQBEKNTRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGPFRV 60
Db 148 VIAGIRETEKFIYVQBEKNTRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGPFRV 207

QY 61 FIGVNDLEREGQMYDNTNP 80
Db 208 FIGVNDLEREGQMYDNTNP 227

RESULT 9
US-09-978-191A-97
Sequence 97, Application US/0978191A
Publication No. US20030050239A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann.
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC4
CURRENT APPLICATION NUMBER: US/09/978,191A
CURRENT FILING DATE: 2001-10-15
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PRIOR FILING DATE: 2001-07-30
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PRIOR FILING DATE: 1998-04-15
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;; PRIOR APPLICATION NUMBER: 60/081952
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085580
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;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.1%; Score 409; DB 10; Length 277;
Best Local Similarity 98.8%; Pred. No. 4.3e-44;
Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VIAGIRETEEKFYIVQEEKNYRESLTHCRIRGGLAMPKDEAANTLIADYVAKSGFFRV 60
DB 148 VIAGIRETEEKFYIVQEEKNYRESLTHCRIRGGLAMPKDEAANTLIADYVAKSGFFRV 207

QY 61 FIGVNDLEREGQYMTDNT 80
DB 208 FIGVNDLEREGQYMTDNT 227

RESULT 10
US-09-978-403A-97
; Sequence 97, Application US/09978403A
; Publication No. US20030050240A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavil, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC17
; CURRENT APPLICATION NUMBER: US/09/978,403A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10

[illegible]

;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.1%; Score 409; DB 10; Length 277;
Best Local Similarity 98.8%; Pred. No. 4.3e-44;
Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VIAGIRETEKEKYIVQEKYVRESLTHCRIRGGMLAMPKDEAAANTLIADYVAKSGFRV 60

Db 148 VIAGIRETEKEKYIVQEKYVRESLTHCRIRGGMLAMPKDEAAANTLIADYVAKSGFRV 207

QY 61 FIGVNDLEREGQYMTDNTP 80

Db 208 FIGVNDLEREGQYMTDNTP 227

RESULT 11

US-09-978-564A-97

;; Sequence 97, Application US/09978564A

;; Publication No. US2003050241A1

;; GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi

;; APPLICANT: Baker, Kevin P.

;; APPLICANT: Botstein, David

;; APPLICANT: Desnoyers, Luc

;; APPLICANT: Eaton, Dan

;; APPLICANT: Ferrara, Napoleon

;; APPLICANT: Filvaroff, Ellen

;; APPLICANT: Fong, Sherman

;; APPLICANT: Gao, Wei-Qiang

;; APPLICANT: Gerber, Hanspeter

;; APPLICANT: Gottard, Audrey

;; APPLICANT: Godowski, Paul J.

;; APPLICANT: Grimaldi, J. Christopher

;; APPLICANT: Gurney, Austin L.

;; APPLICANT: Hillan, Kenneth J.

;; APPLICANT: Kijavini, Ivar J.

;; APPLICANT: Kuo, Sophia S.

;; APPLICANT: Napier, Mary A.

;; APPLICANT: Pan, James

;; APPLICANT: Paoni, Nicholas F.

;; APPLICANT: Roy, Margaret Ann

;; APPLICANT: Shelton, David L.

;; APPLICANT: Stewart, Timothy A.

;; APPLICANT: Tumas, Daniel

;; APPLICANT: Williams, P. Mickey

;; APPLICANT: Wood, William I.

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

;; TITLE OF INVENTION: Acids Encoding the Same

;; FILE REFERENCE: P2630PIC25

;; CURRENT APPLICATION NUMBER: US/09/978,564A

;; CURRENT FILING DATE: 2001-10-16

;; PRIOR APPLICATION NUMBER: 09/918585

;; PRIOR FILING DATE: 2001-07-30

;; PRIOR APPLICATION NUMBER: 60/062250

;; PRIOR FILING DATE: 1997-10-17

;; PRIOR APPLICATION NUMBER: 60/064249

;; PRIOR FILING DATE: 1997-11-03

;; PRIOR APPLICATION NUMBER: 60/065311

;; PRIOR FILING DATE: 1997-11-13

;; PRIOR APPLICATION NUMBER: 60/066364

;; PRIOR FILING DATE: 1997-11-21

;; PRIOR APPLICATION NUMBER: 60/077450

;; PRIOR FILING DATE: 1998-03-10

;; PRIOR APPLICATION NUMBER: 60/077632

;; PRIOR FILING DATE: 1998-03-11

;; PRIOR APPLICATION NUMBER: 60/077641

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; PRIOR APPLICATION NUMBER: 60/085573

; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
Query Match 98.1%; Score 409; DB 10; Length 277;
Best Local Similarity 98.8%; Pred. No. 4.3e-44;
Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VIAGIRETEKFFYIVQEKYRESLTHCRIRGMLAMPKDEAANTLIADYVAKSGFFRV 60
Db 148 VIAGIRETEKFFYIVQEKYRESLTHCRIRGMLAMPKDEAANTLIADYVAKSGFFRV 207
QY 61 FIGVNDLRRGGYMTDNTP 80
Db 208 FIGVNDLRRGGYMTDNTP 227
RESULT 12
US-09-999-833A-97
; Sequence 97, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC65
; CURRENT APPLICATION NUMBER: US/09/999.833A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
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; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11

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3	PRIOR FILING DATE: 1998-04-22	
4	PRIOR APPLICATION NUMBER: 60/082700	
5	PRIOR FILING DATE: 1998-04-22	
6	PRIOR APPLICATION NUMBER: 60/082797	
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8	PRIOR APPLICATION NUMBER: 60/082796	
9	PRIOR FILING DATE: 1998-04-23	
10	PRIOR APPLICATION NUMBER: 60/083336	
11	PRIOR FILING DATE: 1998-04-27	
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30	PRIOR APPLICATION NUMBER: 60/083500	
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32	PRIOR APPLICATION NUMBER: 60/083742	
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34	PRIOR APPLICATION NUMBER: 60/084366	
35	PRIOR FILING DATE: 1998-05-05	
36	PRIOR APPLICATION NUMBER: 60/084414	
37	PRIOR FILING DATE: 1998-05-06	
38	PRIOR APPLICATION NUMBER: 60/084441	
39	PRIOR FILING DATE: 1998-05-06	
40	PRIOR APPLICATION NUMBER: 60/084637	
41	PRIOR FILING DATE: 1998-05-07	
42	PRIOR APPLICATION NUMBER: 60/084639	
43	PRIOR FILING DATE: 1998-05-07	
44	PRIOR APPLICATION NUMBER: 60/084640	
45	PRIOR FILING DATE: 1998-05-07	
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52	PRIOR APPLICATION NUMBER: 60/084643	
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58	PRIOR APPLICATION NUMBER: 60/085562	
59	PRIOR FILING DATE: 1998-05-15	
60	PRIOR APPLICATION NUMBER: 60/085700	
61	PRIOR FILING DATE: 1998-05-15	
62	PRIOR APPLICATION NUMBER: 60/085699	
63	PRIOR FILING DATE: 1998-05-15	
64	PRIOR APPLICATION NUMBER: 60/085573	
65	PRIOR FILING DATE: 1998-05-15	
66	PRIOR APPLICATION NUMBER: 60/085704	
67	PRIOR FILING DATE: 1998-05-15	

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; PRIOR APPLICATION NUMBER: 60/085697
Query Match 98.1%; Score 409; DB 10; Length 277;
Best Local Similarity 98.8%; Pred No. 4.3e-44;
Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VIAGIRETEKYYIVQEBKNTRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFFRV 60
Db 148 VIAGIRETEKYYIVQEBKNTRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFFRV 207
QY 61 FIGVNDLREGQVMTDNTF 80
Db 208 FIGVNDLREGQVMSDNTF 227

RESULT 13
US-09-981-915A-97
; Sequence 97, Application US/09981915A
; Publication No. US20030054986A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630FIC12
; CURRENT APPLICATION NUMBER: US/09/981,915A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
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; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
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Query Match 98.1%; Score 409; DB 10; Length 277;

Best Local Similarity 98.8%; Pred. No. 4.3e-44;
Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 148 VIAGIRETEEEKFYIVQEEKNYRESLTHCIRGGLAMPKDEAANTLIADYVAKSGFFRV 207
QY 61 FIGVNDLEREQYMTDNTTP 80
Db 208 FIGVNDLEREQYMTDNTTP 227
RESULT 14
US-09-978-824-97
; Sequence 37, Application US/09978824
; Publication No. US20030055216A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C14
; CURRENT APPLICATION NUMBER: US/09/978,824
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/918585
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Query Match 98.1%; Score 409; DB 10; Length 277;
Best Local Similarity 98.8%; Pred. No. 4.3e-44;
Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 15

US-09-918-585A-97
; Sequence 97, Application US/09918585A
; Publication No. US20030060406A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
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; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
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; APPLICANT: Kuo, Sophia S.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
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; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C1
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65 PRIOR APPLICATION NUMBER: 60/086023

Query Match 98.1%; Score 409; DB 10; Length 277;
Best Local Similarity 98.8%; Pred.No. 4.3e-44;
Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 VIAGIRETEKFKYIVQEEKYKRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGPRV 60
148 VIAGIRETEKFKYIVQEEKYKRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGPRV 207

Qy
Db

Qy 61 FIGVNDLREGQYMFDTNTP 80
Db 208 FIGVNDLREGQYMTDNT 227

Search completed: March 8, 2004, 12:18:57
Job time : 28.8987 secs